GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:01:46 ; Search time 40.1584 Seconds
(without alignments)
1681.943 Million cell updates/sec

Title: US-10-734-564-72
Perfect score: 3721
Sequence: 1 MESPSAPPHRWCIPWQRLLL.....LSAGATVGIMIGVLVGVALI 702

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3721	100.0	702	2	A36319	carcinoembryonic a
2	1609	43.2	526	1	A32164	biliary glycoprote
3	1600.5	43.0	464	2	C30127	transmembrane carc
4	1589.5	42.7	417	2	JH0394	biliary glycoprote
5	1470	39.5	286	2	A28333	carcinoembryonic a
6	1443	38.8	344	2	A27681	nonspecific cross-
7	1427	38.3	351	2	JH0396	biliary glycoprote
8	1423	38.2	321	2	JH0395	biliary glycoprote
9	1272	34.2	349	2	A34815	carcinoembryonic a
10	1157.5	31.1	428	2	JS0032	pregnancy-specific
11	1148.5	30.9	419	2	JC4123	pregnancy-specific
12	1141.5	30.7	428	2	I57486	pregnancy-specific
13	1133.5	30.5	428	2	A27658	pregnancy-specific
14	1130	30.4	436	2	B55181	pregnancy-specific
15	1127.5	30.3	426	2	A35964	pregnancy-specific
16	1127.5	30.3	426	2	S09016	pregnancy-specific
17	1127.5	30.3	426	2	A35341	pregnancy-specific
18	1127.5	30.3	495	2	A55181	pregnancy-specific
19	1126.5	30.3	417	2	A28277	pregnancy-specific
20	1126.5	30.3	419	2	A31135	pregnancy-specific
21	1126.5	30.3	426	2	C55181	pregnancy-specific
22	1126.5	30.3	426	2	B35334	pregnancy-specific
23	1125.5	30.2	426	2	B33258	pregnancy-specific
24	1124.5	30.2	419	2	A33258	pregnancy-specific
25	1117.5	30.0	419	2	B54312	pregnancy-specific
26	1107.5	29.8	435	2	D33258	pregnancy-specific
27	1106.5	29.7	419	2	A36109	pregnancy-specific
28	1099	29.5	424	2	A34595	pregnancy-specific
29	1085.5	29.2	406	2	E43354	pregnancy-specific
30	1080.5	29.0	395	2	D43354	pregnancy-specific
31	1078.5	29.0	397	2	C43354	pregnancy-specific
32	1070.5	28.8	521	2	S34338	biliary glycoprote
33	1069.5	28.7	458	2	JC1509	biliary glycoprote
34	1069	28.7	424	2	B36109	pregnancy-specific
35	1023.5	27.5	521	2	JC1508	biliary glycoprote
36	1018.5	27.4	458	1	WMMSR1	biliary glycoprote
37	988.5	26.6	519	2	A44783	ecto-ATPase precur
38	983	26.4	458	2	S68177	C-CAM2a protein is
39	965	25.9	458	2	S23969	cell-adhesion mole
40	919	24.7	402	2	A54312	pregnancy-specific
41	900.5	24.2	352	2	I77374	pregnancy-specific
42	898	24.1	332	2	JN0067	pregnancy-specific
43	892	24.0	335	2	H43354	pregnancy-specific
44	890	23.9	335	2	A33514	pregnancy-specific
45	889	23.9	326	2	JC4124	pregnancy-specific

ALIGNMENTS

RESULT 1
A36319
carcinoembryonic antigen precursor - human
N;Alternate names: CEA; meconium antigen 100
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098;
R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shivel
Mol. Cell. Biol. 10, 2738-2748, 1990
A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its p
A;Reference number: A36319; MUID:90258861; PMID:2342461
A;Accession: A36319
A;Molecule type: DNA
A;Residues: 1-702 <SCH>
A;Cross-references: UNIPROT:P06731; UNIPARC:UPI000003AE4C; GB:M17303; NID:g178676; PI
A;Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-T
R;Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P.
Mol. Cell. Biol. 7, 3221-3230, 1987
A;Title: Isolation and characterization of full-length functional cDNA clones for hum
A;Reference number: A27773; MUID:88038876; PMID:3670312
A;Accession: A27773
A;Molecule type: mRNA
A;Residues: 1-702 <BEA>
A;Cross-references: UNIPARC:UPI000003AE4C; GB:M29540; NID:g180222; PIDN:AAA51967.1;
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA a
A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: A31037
A;Molecule type: mRNA
A;Residues: 1-702 <BAR>
A;Cross-references: UNIPARC:UPI000003AE4C; GB:M29540; NID:g180222; PIDN:AAA51967.1;
A;Note: the authors translated the codon GTG for residue 130 as Leu
R;Oikawa, S.; Nakazato, H.; Kosaki, G.
Biochem. Biophys. Res. Commun. 142, 511-518, 1987
A;Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA
A;Reference number: A25845; MUID:87128144; PMID:3814146
A;Accession: A25845
A;Molecule type: mRNA
A;Residues: 5-702 <OIK>
A;Cross-references: UNIPARC:UPI000011D6BE; GB:M15042; NID:g180198; PIDN:AAA51963.1;
R;Oikawa, S.
submitted to the EMBL Data Library, September 1989
A;Reference number: S08106
A;Accession: S08106
A;Molecule type: mRNA
A;Residues: 5-319,321-702 <OI2>
A;Cross-references: UNIPARC:UPI000016A69F; EMBL:X16455; NID:g29854; PIDN:CAA34474.1;
R;Barnett, T.
submitted to the EMBL Data Library, September 1991
A;Description: Genomic DNA sequence upstream of the translational start of the carci
A;Reference number: S31737

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A;Accession: S31737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <BA2>
A;Cross-references: UNIPARC:UPI0000177089; EMBL:X62151
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembr
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: A44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
A;Cross-references: UNIPARC:UPI000017708A
R;Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A;Title: Characterization of the genomic organization of human carcinoembryonic antigen
A;Reference number: I54224; MUID:91139118; PMID:2286372
A;Accession: I54224
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: UNIPARC:UPI000016A69E; GB:M60964; NID:g180215; PIDN:AAA51964.1; PID:
R;Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A;Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon
A;Reference number: I59098; MUID:87204247; PMID:3033671
A;Accession: I59098
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 331-702 <RE2>
A;Cross-references: UNIPARC:UPI000016A6A0; GB:M16234; NID:g180240; PIDN:AAA51972.1; PID:
R;Siepen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
Biochem. Biophys. Res. Commun. 147, 212-218, 1987
A;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105
A;Reference number: A26831; MUID:87326349; PMID:3632664
A;Accession: A26831
A;Molecule type: protein
A;Residues: 35-64 <SIE>
A;Cross-references: UNIPARC:UPI000017708B
R;Thomas, P.; Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A;Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at t
A;Reference number: A35490; MUID:90321257; PMID:2372297
A;Accession: A35490
A;Molecule type: protein
A;Residues: 'X',140-151,'X',153,'X',155-156 <THO>
A;Cross-references: UNIPARC:UPI000017708C
A;Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer
C;Comment: This heavily glycosylated membane protein of unknown function is a widely use
C;Comment: This protein may be processed at its C-terminus. It is anchored to the membra
C;Genetics:
A;Gene: GDB:CEA
A;Cross-references: GDB:119054; OMIM:114890
A;Map position: 19q13.2-19q13.2
A;Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-678/Product: carcinoembryonic antigen #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;338-395/Domain: immunoglobulin homology <IMM3>
F;516-573/Domain: immunoglobulin homology <IMM4>
F;608-657/Domain: immunoglobulin homology <IMM5>
F;679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

  Query Match           100.0%;  Score 3721;  DB 2;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-194;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
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Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
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Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 2
A32164
biliary glycoprotein 1 precursor, splice form a - human
N;Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane ca
N;Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form .
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476
R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,
Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
A;Reference number: A32164
A;Contents: erratum
A;Accession: A32164
A;Molecule type: mRNA
A;Residues: 1-526 <HIN>
A;Cross-references: UNIPROT:P13688; UNIPARC:UPI0000127483; GB:J03858; NID:g179439; PIDN
R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,
Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
A;Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of
A;Reference number: A94206; MUID:88320555; PMID:2457922
A;Contents: annotation
A;Note: the sequence shown in this reference has been completely corrected in reference
R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J , K
J. Cell Biol. 108, 267-276, 1989
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A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
A;Reference number: A92752; MUID:89139550; PMID:2537311
A;Accession: A30127
A;Molecule type: mRNA
A;Residues: 1-526 <BAR1>
A;Cross-references: UNIPARC:UPI0000127483; EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PID
A;Experimental source: splice form a
A;Accession: B30127
A;Molecule type: mRNA
A;Residues: 1-319,'D',417-526 <BAR2>
A;Cross-references: UNIPARC:UPI0000073D2E; EMBL:X14831; NID:g37199; PIDN:CAA32940.1; PID
A;Experimental source: splice form b
R;Barnett, T.R.; Drake, L.; Pickle II, W.
Mol. Cell. Biol. 13, 1273-1282, 1993
A;Title: Human biliary glycoprotein gene: characterization of a family of novel alternat
A;Reference number: A48078; MUID:93140765; PMID:8423792
A;Accession: A48078
A;Molecule type: mRNA
A;Residues: 124-141,'H',417-526 <BAR3>
A;Cross-references: UNIPARC:UPI0000173868; GB:M76742; NID:g179480; PIDN:AAA57142.1; PID:
A;Experimental source: splice form x
A;Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBIP:123606)
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
R;Hauck, W.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N.
Eur. J. Biochem. 223, 529-541, 1994
A;Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami
A;Reference number: S45664; MUID:94333343; PMID:8055923
A;Accession: S45664
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-21 <HAU>
A;Cross-references: UNIPARC:UPI000006E9AC; EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID
R;Nedellec, P.; Turbide, C.; Beauchemin, N.
Eur. J. Biochem. 231, 104-114, 1995
A;Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A;Reference number: S65939; MUID:95354678; PMID:7628460
A;Accession: S65939
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-21 <NED>
A;Cross-references: UNIPARC:UPI000006E9AC; EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A;Note: only a part of the coding sequence is given
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembr
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Contents: annotation; alignment of related sequences
C;Genetics:
A;Gene: GDB:BGP
A;Cross-references: GDB:127992; OMIM:109770
A;Map position: 19q13.2-19q13.2
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
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F;35-428/Domain: extracellular #status predicted <EXT>
F;35-319,'D',417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M
F;35-141,'H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted <M
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>
F;425-454/Domain: transmembrane #status predicted <TMM>
F;453-526/Domain: intracellular #status predicted <INT>
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  Query Match            43.2%;  Score 1609;  DB 1;  Length 526;
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  Matches  326;  Conservative   47;  Mismatches  121;  Indels   26;  Gaps    6;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| ||||||||||||||||:|| || ||||||||||||||||||| |||

Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |||||||||||||||:|| |||||||||| |||| ||||||||||: |||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              ||||||||||||| |||||||||||||| |||||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
              :| || | ||:|||:|||||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
              || ||||| || |    |   || | :: :   |:|:| |||      :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
              ||| | |::|| | ||::  | | | | | | : | :| : |||::||| |   | :
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDG---------NIQQHTQELFISNITEK 470
              :||       |: : :   |    |   :|  |         :: :|     :|| |:
Db        425 LSPGAI---AGIVIGVVALVALIAVALACFLHFGKTGRASDQRDLTEHKPS--VSNHTQD 479

Qy        471 NSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNS 510
              :|       |:  :  :  |  |:   |: |    |:: |
Db        480 HS-------NDPPNKMNEVTYSTLNFEAQQPTQPTSASPS 512


RESULT 3
C30127
transmembrane carcinoembryonic antigen 3 precursor - human
N;Alternate names: CD66 splice form BGPc
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: C30127; I52597
R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J J.
J. Cell Biol. 108, 267-276, 1989
A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple u
A;Reference number: A92752; MUID:89139550; PMID:2537311
A;Accession: C30127
A;Molecule type: mRNA
A;Residues: 1-464 <BAR>
A;Cross-references: UNIPROT:Q16170; UNIPARC:UPI0000072309; EMBL:X16356; EMBL:X14784
R;Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Gschmeissner, S.E.; Hajib
Blood 84, 200-210, 1994
A;Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning,
A;Reference number: I52597; MUID:94289702; PMID:8018919
A;Accession: I52597
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-464 <RES>
A;Cross-references: UNIPARC:UPI0000072309; GB:S71326; NID:g550030; PIDN:AAB31183.1,
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-t
C;Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane prot
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>
F;424-455/Domain: transmembrane #status predicted <TMM>
F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405/

  Query Match            43.0%;  Score 1600.5;  DB 2;  Length 464;
  Best Local Similarity  73.0%;  Pred. No. 9.1e-80;
  Matches  309;  Conservative   30;  Mismatches   79;  Indels    5;  Gaps    2;
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Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
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Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
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Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
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Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
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Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
              || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
              ||| | |::||  | ||::  | | | | | | : | :| : |||::||| |   | :
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISP 422
              :||
Db        425 LSP 427


RESULT 4
JH0394
biliary glycoprotein g precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0394
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0394
A;Molecule type: mRNA
A;Residues: 1-417 <KUR>
A;Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A624; GB:M72238; NID:g179436; PIDN:
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-383/Product: biliary glycoprotein g #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>

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  Matches  305;  Conservative   28;  Mismatches   74;  Indels    3;  Gaps    1;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
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Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |||||||||||||||:|| |||||||||| |||| |||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
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Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
               :| || | ||:|||:|||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
              || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNV 411
              ||| | |::||  | ||::  | | | | | | : | :| : |||::|||
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNV 414


RESULT 5
A28333
carcinoembryonic antigen-related protein (clone eLV7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: A28333
R;Kamarck, M.E.; Elting, J.J.; Hart, J.T.; Goebel, S.J.; Rae, P.M.M.; Nothdurft, M.A
Proc. Natl. Acad. Sci. U.S.A. 84, 5350-5354, 1987
A;Title: Carcinoembryonic antigen family: expression in a mouse L-cell transfectant a
A;Reference number: A28333; MUID:87260984; PMID:2955415
A;Accession: A28333
A;Molecule type: mRNA
A;Residues: 1-286 <KAM>
A;Cross-references: UNIPROT:Q13984; UNIPARC:UPI0000177090
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-te
F;23-80/Domain: immunoglobulin homology <IMM1>
F;115-164/Domain: immunoglobulin homology <IMM2>
F;201-258/Domain: immunoglobulin homology <IMM3>

  Query Match             39.5%;  Score 1470;  DB 2;  Length 286;
  Best Local Similarity   98.6%;  Pred. No. 5.8e-73;
  Matches  276;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        322 PPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLL 381
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 PIKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLL 66

Qy        382 SVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAAS 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        442 NPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELP 501
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Qy        502 KPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNV 561
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Db        187 KPSISSNNSKPVEDKDAVAFHCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNV 246

Qy        562 TRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPP 601
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Db        247 TRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPP 286


RESULT 6
A27681
nonspecific cross-reacting antigen precursor - human
N;Alternate names: NCA; TEX/NCA
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476, F44
R;Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
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A;Reference number: A26902; MUID:87298464; PMID:3619891
A;Accession: A26902
A;Molecule type: DNA
A;Residues: 1-141 <OIK>
A;Cross-references: UNIPROT:Q13774; UNIPARC:UPI0000072416; GB:M17082; NID:g180230; PIDN:
R;Thompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, C
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
A;Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami
A;Reference number: A29875; MUID:87204248; PMID:3033672
A;Accession: A29875
A;Molecule type: DNA
A;Residues: 23-141 <THO>
A;Cross-references: UNIPARC:UPI0000177070; GB:M16337
A;Note: the authors translated the codon ACT for residue 64 as Tyr
R;Tawaragi, Y.; Oikawa, S.; Matsuoka, Y.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 150, 89-96, 1988
A;Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carci
A;Reference number: A27681; MUID:88106638; PMID:3337731
A;Accession: A27681
A;Molecule type: mRNA
A;Residues: 1-238,'V',240-344 <TAW>
A;Cross-references: UNIPARC:UPI000012748C; GB:M18728; NID:g189084; PIDN:AAA59907.1; PID:
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: B31037
A;Molecule type: mRNA
A;Residues: 1-137,'L',139-344 <BAR>
A;Cross-references: UNIPARC:UPI000016ADC6; GB:M29541; NID:g189103; PIDN:AAA59915.1; PID:
A;Note: the authors translated the codon TTG for residue 138 as Phe
R;Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A;Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC
A;Reference number: A29918; MUID:88139389; PMID:2830274
A;Accession: A29918
A;Molecule type: mRNA
A;Residues: 1-344 <NEU>
A;Cross-references: UNIPARC:UPI000006DF42; GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51
R;Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind
A;Reference number: A27709; MUID:88268882; PMID:3390172
A;Accession: A27709
A;Molecule type: protein
A;Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-235
A;Cross-references: UNIPARC:UPI0000177071; UNIPARC:UPI0000177072; UNIPARC:UPI0000177073;
078; UNIPARC:UPI0000177079; UNIPARC:UPI000017707A
R;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci
A;Reference number: A36271; MUID:90256782; PMID:2341397
A;Accession: A36271
A;Molecule type: protein
A;Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;310
A;Cross-references: UNIPARC:UPI000017707B; UNIPARC:UPI000017707C; UNIPARC:UPI000017707D;
082; UNIPARC:UPI0000177083; UNIPARC:UPI0000177084
R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A;Reference number: A26414; MUID:87147209; PMID:3469650
A;Accession: C26414
A;Molecule type: protein
A;Residues: 35-69 <PAX>
A;Cross-references: UNIPARC:UPI0000177085
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembr
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: E44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
A;Cross-references: UNIPARC:UPI0000177086
A;Accession: F44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-137,'L',139-141 <KH2>
A;Cross-references: UNIPARC:UPI0000177086
C;Comment: This protein appears to be processed at the carboxyl terminus and anchored
C;Genetics:
A;Gene: GDB:NCA
A;Cross-references: GDB:120221; OMIM:163980
A;Map position: 19q13.2-19q13.2
A;Introns: 22/1
A;Note: the list of introns may be incomplete
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosph
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (coval
F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature f

Query Match 38.8%; Score 1443; DB 2; Length 344;
Best Local Similarity 83.9%; Pred. No. 2.1e-71;
Matches 271; Conservative 11; Mismatches 41; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
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Db          1 MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  |||||||||||||  |:||||||||||||||||| ||||||||||: |||||||
Db         61 NRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              || |||||||||||||| |||||||||||||| |||||||||||||| |: ||||||
Db        121 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              | |||||||||||||||| |||| :| |||  ||:|| ||| || ||| | ||||||||
Db        181 NGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
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Db        241 TISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFQQSTQELFIPNITVNNSGSYMCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPP 323
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Db        301 AHNSATGLNRTTVTMITVSGSAP 323
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RESULT 7
JH0396
biliary glycoprotein i precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0396
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clone
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0396
A;Molecule type: mRNA
A;Residues: 1-351 <KUR>
A;Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A626; GB:M72238; NID:g179436; I
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-te
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

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F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-351/Product: biliary glycoprotein i #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

  Query Match             38.3%;  Score 1427;  DB 2;  Length 351;
  Best Local Similarity   84.6%;  Pred. No. 1.6e-70;
  Matches  269;  Conservative   12;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||||:|| || ||||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              ||||||||||||||:|| |||||||||| |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
               :| || | ||:|||:|||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEP 322
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Db        305 VTGCNRTTVKTIIVTESP 322


RESULT 8
JH0395
biliary glycoprotein h precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0395
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0395
A;Molecule type: mRNA
A;Residues: 1-321 <KUR>
A;Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A625; GB:M69176; NID:g179434; PIDN:
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-321/Product: biliary glycoprotein h #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

  Query Match             38.2%;  Score 1423;  DB 2;  Length 321;
  Best Local Similarity   85.4%;  Pred. No. 2.4e-70;
  Matches  268;  Conservative   12;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||||:|| || ||||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              ||||||||||||||:|| |||||||||| |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
               :| || | ||:|||:|||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITV 318
              || ||||| || |
Db        305 VTGCNRTTVKTIIV 318


RESULT 9
A34815
carcinoembryonic antigen family member CGM6 precursor - human
N;Alternate names: carcinoembryonic antigen family member NCA-95; CD67; nonspecific c
C;Species: Homo sapiens (man)
C;Date: 13-Jul-1990 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: S13524; I44476; A34815
R;Berling, B.; Kolbinger, F.; Grunert, F.; Thompson, J.A.; Brombacher, F.; Buchegger,
Cancer Res. 50, 6534-6539, 1990
A;Title: Cloning of a carcinoembryonic antigen gene family member expressed in leukocy
A;Reference number: S13524; MUID:91003998; PMID:2208113
A;Accession: S13524
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-349 <BER>
A;Cross-references: UNIPROT:P31997; UNIPARC:UPI000016A6BD; EMBL:X52378; NID:g29918; PI
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoem
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: I44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
A;Cross-references: UNIPARC:UPI000017708D
R;Arakawa, F.; Kuroki, M.; Misumi, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 166, 1063-1071, 1990
A;Title: Characterization of a cDNA clone encoding a new species of the nonspecific crc
A;Reference number: A34815; MUID:90165902; PMID:2306228
A;Accession: A34815
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113,'R',115-321,'V',323-349 <ARA>
A;Cross-references: UNIPARC:UPI000016ADC5; GB:D90064; NID:g219935; PIDN:BAA14108.1; PID
A;Experimental source: white blood cells
C;Genetics:
A;Gene: GDB:CGM6
A;Cross-references: GDB:127667
A;Map position: 19q13.2-19q13.2
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term
C;Keywords: phosphatidylinositol linkage
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

  Query Match             34.2%;  Score 1272;  DB 2;  Length 349;
  Best Local Similarity   76.8%;  Pred. No. 4.1e-62;
  Matches  241;  Conservative   19;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              |||  || |||| ||||||| |||||||||:||||: | | |||||||||||||||   |
Db          5 SAPSCRWRIPWQGLLLTASLFTFWNPPTTAQLTIEAVPSNAAEGKEVLLLVHNLPQDPRG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |:||||| || ||:|||||  || ||||||| || ||||||||::|: :|||| ||| |
Db         65 YNWYKGETVDANRRIIGYVISNQQITPGPAYSNRETIYPNASLLMRNVTKNDTGSYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              || :|::|| |||| |:|| |||||||||| |||||||||||||||: ||||||| ||
```

```
Db        125 IKLNLMSEEVTGQFSVHPETPKPSISSNNSNPVEDKDAVAFTCEPETQNTTYLWWVNGQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||   |:|| ||| ||  || | ||||||||||||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDVGPYECEIQNPASANFSDPVTLNVLYGPDAPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
              :| | :| ||||||||||||||:|||| ||||||| ||:|||||||  ||||| |   ||
Db        245 SDTYYHAGVNLNLSCHAASNPPSQYSWSVNGTFQQYTQKLFIPNITTKNSGSYACHTTNS 304

Qy        305 DTGLNRTTVTTITV 318
              || |||||  |||
Db        305 ATGRNRTTVRMITV 318


RESULT 10
JS0032
pregnancy-specific beta-1 glycoprotein 3 precursor - human
N;Alternate names: pregnancy-specific beta-1 glycoprotein A precursor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JS0032; PS0308; A32719; C35341; B34647; A35334
R;Rooney, B.C.; Horne, C.H.W.; Hardman, N.
Gene 71, 439-449, 1988
A;Title: Molecular cloning of a cDNA for human pregnancy-specific beta 1-glycoprotein: h
A;Reference number: JS0032; MUID:89138020; PMID:3265688
A;Accession: JS0032
A;Molecule type: mRNA
A;Residues: 1-428 <ROO>
A;Cross-references: UNIPROT:Q16557; UNIPARC:UPI000002D1C2; GB:M23575; NID:g183596; PIDN:
A;Accession: PS0308
A;Molecule type: protein
A;Residues: 50-69;99-113;160-167;210-216;266-275;337-344 <RO2>
A;Cross-references: UNIPARC:UPI00001770A1; UNIPARC:UPI00001770A2; UNIPARC:UPI00001770A3;
R;Streydio, C.; Swillens, S.; Georges, M.; Szpirer, C.; Vassart, G.
Genomics 6, 579-592, 1990
A;Title: Structure, evolution and chromosomal localization of the human pregnancy-specif
A;Reference number: A32719; MUID:90256167; PMID:2341148
A;Accession: A32719
A;Molecule type: mRNA
A;Residues: 1-428 <STR>
A;Cross-references: UNIPARC:UPI000002D1C2; GB:M34420; NID:g183594; PIDN:AAA52606.1; PID:
R;Zoubir, F.; Khan, W.N.; Hammarstroem, S.
Biochem. Biophys. Res. Commun. 169, 203-216, 1990
A;Title: Carcinoembryonic antigen gene family members in submandibular salivary gland: d
A;Reference number: A35341; MUID:90274668; PMID:2350345
A;Accession: C35341
A;Molecule type: mRNA
A;Residues: 1-428 <ZOU>
A;Cross-references: UNIPARC:UPI000002D1C2; GB:M37399; NID:g180234; PIDN:AAA60958.1; PID:
A;Note: the sequence shown differs from the translation of the nucleotide shown in the r
R;Borjigin, J.; Tease, L.A.; Barnes, W.; Chan, W.Y.
Biochem. Biophys. Res. Commun. 166, 622-629, 1990
A;Title: Expression of the pregnancy-specific beta 1-glycoprotein genes in human testis.
A;Reference number: A34647; MUID:90147764; PMID:2302228
A;Accession: B34647
A;Molecule type: mRNA
A;Residues: 23-329;384-428 <BOR>
A;Cross-references: UNIPARC:UPI00001770A7; UNIPARC:UPI00001770A8
A;Note: the mRNA sequenced here has both a deletion and an unspliced intron
C;Comment: This protein plays an essential role in normal pregnancy. It is a well-charac
ells.
C;Genetics:
A;Gene: GDB:PSG3
A;Cross-references: GDB:128239; OMIM:176392
A;Map position: 19q13.2-19q13.2
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; membrane protein; tandem repeat
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-428/Product: pregnancy-specific beta-1-glycoprotein #status predicted <MAT>
F;162-219/Domain: immunoglobulin homology <IMM1>
F;255-312/Domain: immunoglobulin homology <IMM2>
F;347-396/Domain: immunoglobulin homology <IMM3>
F;104,111,268,303/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           31.1%;  Score 1157.5;  DB 2;  Length 428;
  Best Local Similarity  47.8%;  Pred. No. 8.7e-56;
  Matches  237;  Conservative   51;  Mismatches  121;  Indels   87;  Gaps    3;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||||    | |: |||||||| ||||||||::|||: |  |::||:|||||||||:| |
Db          5 SAPPCTQRITWKGLLLTASLLNFWNPPTTAQVTIEAEPTKVSKGKDVLLLVHNLPQNLAG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              | ||||:  |    |  ||:  |    |||||||| :| ||||||||: : | | ||||:
Db         65 YIWYKGQMKDLYHYITSYVVDGQIIIYGPAYSGRETVYSNASLLIQNVTREDAGSYTLHI 124

Qy        125 IKSDLVNEEATGQ--FRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNN 182
              :|         ||   | :| | |||||||:|  | || :||: ||:||| ||:||||:|
Db        125 VKRGDGTRGETGHFTFTLYLETPKPSISSSNLYPREDMEAVSLTCDPETPDASYLWWMNG 184

Qy        183 QSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTI 242
              ||||::  ||||   ||| || ||:     |:|| :||||| ||| | ||:|
Db        185 QSLPMTHSLQLSKNKRTLFLFGVTKYTAGPYECEIRNPVSASRSDPVTLNLL-------- 236

Qy        243 SPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAH 302
                                                          | :
Db        237 ----------------------------------------------PKL---------- 239

Qy        303 NSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQS 362
                                  |||:|| || || |::| :| ||||: :| ||:||:| ||
Db        240 --------------------PKPYITINNLNPRENKDVLAFTCEPKSENYTYIWWLNGQS 279

Qy        363 LPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISP 422
              ||||||::   :|| | | |||||: |||:| ||:      | || ||||||| | | |
Db        280 LPVSPRVKRPIENRILILPSVTRNETGPYQCEIQDRYGGIRSYPVTLNVLYGPDLPRIYP 339

Qy        423 SYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNS 482
              |:||| | || ||| | |||||:||| |:|  |   |:|||  || |:|||| |   ||
Db        340 SPTYYHSGENLYLSCFADSNPPAEYSWTINGKFQLSGQKLFIPQITTKHSGLYACSVRNS 399

Qy        483 ASGHSRTTVKTITVSA 498
              |:|   :   |: |||
Db        400 ATGMESSKSMTVKVSA 415


RESULT 11
JC4123
pregnancy-specific glycoprotein 7a precursor - human
C;Species: Homo sapiens (man)
C;Date: 26-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JC4123
R;Teglund, S.; Zhou, G.Q.; Hammarstroem, S.
Biochem. Biophys. Res. Commun. 211, 656-664, 1995
A;Title: Characterization of cDNA encoding novel pregnancy-specific glycoprotein vari
A;Reference number: JC4121; MUID:95314639; PMID:7794280
A;Accession: JC4123
A;Molecule type: mRNA
A;Residues: 1-419 <TEG>
A;Cross-references: UNIPROT:Q13046; UNIPARC:UPI00001327A2; GB:U18467; NID:g609313; PI
A;Experimental source: fetal liver
C;Comment: This protein belongs to the carcinoembryonic antigen family. This protein
egnancy.
C;Genetics:
A;Gene: GDB:PSG7
A;Cross-references: GDB:128241; OMIM:176396
A;Map position: 19q13.2-19q13.2
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
C;Keywords: glycoprotein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-419/Product: pregnancy-specific glycoprotein 7a #status predicted <MAT>
F;127-129/Region: cell attachment (R-G-D) motif
F;162-219/Domain: immunoglobulin homology <IMM1>
F;255-312/Domain: immunoglobulin homology <IMM2>
```

```
F;347-396/Domain: immunoglobulin homology <IMM3>
F;61,104,111,199,209,268,303/Binding site: carbohydrate (Asn) (covalent) #status predict

  Query Match            30.9%;  Score 1148.5;  DB 2;  Length 419;
  Best Local Similarity  48.1%;  Pred. No. 2.6e-55;
  Matches  238;  Conservative   47;  Mismatches  123;  Indels   87;  Gaps    3;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||||    | |: |||||||| |||||||||::|||: |  |:|||:||||||||||:| |
Db          5 SAPPCTQHITWKGLLLTASLLNFWNPPTTAQVTIEAQPPKVSEGKDVLLLVHNLPQNLTG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              | ||||:  |    :  ||:  |    |||||||| :| ||||||||: | ||| ||||:
Db         65 YIWYKGQIRDLYHYVTSYVVDGQIIKYGPAYSGRETVYSNASLLIQNVTQEDTGSYTLHI 124

Qy        125 IKSDLVNEEATGQ--FRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNN 182
              ||         ||:  | :| | |||||||:|  | |  :||  ||:||| ||:|||||:|
Db        125 IKRGDGTGGVTGRFTFTLYLETPKPSISSSNFNPREATEAVILTCDPETPDASYLWWMNG 184

Qy        183 QSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTI 242
              ||||::  ||||  |||| || ||       |:|| :||||| ||| | ||:|
Db        185 QSLPMTHSLQLSETNRTLYLFGVTNYTAGPYECEIRNPVSASRSDPVTLNLL-------- 236

Qy        243 SPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAH 302
                                                    | :
Db        237 ---------------------------------------------PKL------------ 239

Qy        303 NSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQS 362
                              |||:|| || || |::|    ||||: :| ||:||:| ||
Db        240 --------------------PKPYITINNLNPRENKDVSTFTCEPKSENYTYIWWLNGQS 279

Qy        363 LPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISP 422
              ||||||::   :|| | | |||||: |||:| |::       ||||  |||||||| | | |
Db        280 LPVSPRVKRRIENRILILPSVTRNETGPYQCEIRDRYGGIRSDPVTLNVLYGPDLPRIYP 339

Qy        423 SYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNS 482
              |:|||  | || ||| | |||||||||| |:|  |   |:| |  || |:|||| |   ||
Db        340 SFTYYHSGQNLYLSCFADSNPPAQYSWTINGKFQLSGQKLSIPQITTKHSGLYACSVRNS 399

Qy        483 ASGHSRTTVKTITVS 497
              |:|   :   |: ||
Db        400 ATGKESSKSVTVRVS 414


RESULT 12
I57486
pregnancy-specific beta 1-glycoprotein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I57486
R;Shupert, W.L.; Chan, W.Y.
Mol. Cell. Biochem. 120, 159-170, 1993
A;Title: Pregnancy specific beta 1-glycoprotein in human intestine.
A;Reference number: I57486; MUID:93254418; PMID:8487756
A;Accession: I57486
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-428 <RES>
A;Cross-references: UNIPARC:UPI0000073DC1; GB:S59493; NID:g300090; PIDN:AAC60584.1; PID:
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;347-396/Domain: immunoglobulin homology <IMM>

  Query Match            30.7%;  Score 1141.5;  DB 2;  Length 428;
  Best Local Similarity  47.4%;  Pred. No. 6.4e-55;
  Matches  235;  Conservative   51;  Mismatches  123;  Indels   87;  Gaps    3;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||||    | |: ||||| || ||| ||||::|||: |  |::||:|||||||||:| |
Db          5 SAPPCTQRITWKGLLLTALLLNFWNLPTTAQVTIEAEPTKVSKGKDVLLLVHNLPQNLAG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              | ||||:  |    :  ||:  |    |||||||| :| ||||||||: | ||| ||||:
Db         65 YIWYKGQMKDLYHYITSYVVDGQIIIYGPAYSGRETVYSNASLLIQNVTREDAGSYTLHI 124

Qy        125 IKSDLVNEEATGQ--FRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNN 182
              :|         ||    | :| | |||||||:|  | || :||: ||:||| ||:|||:|
Db        125 VKRGDGTRGETGHFTFTLYLETPKPSISSSNLYPREDMEAVSLTCDPETPDASYLWWMNG 184

Qy        183 QSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTI 242
              ||||::  ||||   ||| || ||:     |:|| :||||| ||| | ||:|
Db        185 QSLPMTHSLQLSKNKRTLFLFGVTKYTAGPYECEIRNPVSASRSDPVTLNLL-------- 236

Qy        243 SPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAH 302
                                                    | :
Db        237 ---------------------------------------------PKL------------ 239

Qy        303 NSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQS 362
                              |||:|| || || |::| :| |||: :| ||:||:| ||
Db        240 --------------------PKPYITINNLNPRENKDVLAFTCEPKSENYTYIWWLNGQS 279

Qy        363 LPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISP 422
              ||||||::   :|| | | |||||: |||:| |::       |||| |||||||| | | |
Db        280 LPVSPRVKRPIENRILILPSVTRNETGPYQCEIQDRYGGIRSYPVTLNVLYGPDLPRIYP 339

Qy        423 SYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNS 482
              |:|||  | || ||| | |||||:||| |:|   |    |:|||  || |:|||| |   ||
Db        340 SFTYYHSGENLYLSCFADSNPPAEYSWTINGKFQLSGQKLFIPQITTKHSGLYACSVRNS 399

Qy        483 ASGHSRTTVKTITVSA 498
              |:|   :   |: |||
Db        400 ATGMESSKSMTVKVSA 415


RESULT 13
A27658
pregnancy-specific beta-1 glycoprotein C precursor - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 30-Jun-1991 #text_change 31-Oct-1997
C;Accession: A27658
R;Streydio, C.; Lacka, K.; Swillens, S.; Vassart, G.
Biochem. Biophys. Res. Commun. 154, 130-137, 1988
A;Title: The human pregnancy-specific beta-1-glycoprotein (PS-beta-G) and the carcinoem
A;Reference number: A27658; MUID:88280756; PMID:3260773
A;Accession: A27658
A;Molecule type: mRNA
A;Residues: 1-428 <STR>
A;Cross-references: UNIPARC:UPI000006DB43; GB:M19662
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C;Keywords: glycoprotein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-428/Product: pregnancy-specific beta-1 glycoprotein C #status predicted <MAT>
F;162-219/Domain: immunoglobulin homology <IMM1>
F;255-312/Domain: immunoglobulin homology <IMM2>
F;347-396/Domain: immunoglobulin homology <IMM3>

  Query Match            30.5%;  Score 1133.5;  DB 2;  Length 428;
  Best Local Similarity  46.4%;  Pred. No. 1.7e-54;
  Matches  237;  Conservative   56;  Mismatches  131;  Indels   87;  Gaps    3;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              | : ||||    | |: |||||||| ||| ||||::|||: |  |:|||:|||||||||
Db          1 MGTLSAPPCTQRIKWKGLLLTASLLNFWNLPTTAQVTIEAEPTKVSEGKDVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :| || ||||:  |    |  ||:  :    |||||||  | ||||||||: : | | |
Db         61 NLTGYIWYKGQMRDLYHYITSYVVDGEIIIYGPAYSGRETAYSNASLLIQNVTREDAGSY 120

Qy        121 TLHVIKSDLVNEEATGQ--FRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLW 178
              |||:|| |       ||:  | :: | |||||||:|  | |  :||: ||:||| ||:|||
Db        121 TLHIIKGDDGTRGVTGRFTFTLHLETPKPSISSSNLNPRETMEAVSLTCDPETPDASYLW 180

Qy        179 WVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPD 238
              |:| ||||::  |:||  |||| |  ||:     |:|| :||||| ||| | ||:|
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Db        181 WMNGQSLPMTHSLKLSETNRTLFLLGVTKYTAGPYECEIRNPVSASRSDPVTLNLL---- 236

Qy        239 APTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYT 298
                                                                  | :
Db        237 ----------------------------------------------------PKL--------- 239

Qy        299 CQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWV 358
                                      |||:|| || || |::| :  ||||: :| ||:||:
Db        240 ----------------------PKPYITINNLNPRENKDVLNFTCEPKSENYTYIWWL 275

Qy        359 NNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDP 418
              | ||||||||::   :|| | | |||||: |||:| |::       |||| |||||||| |
Db        276 NGQSLPVSPRVKRPIENRILILPSVTRNETGPYQCEIRDRYGGIRSDPVTLNVLYGPDLP 335

Qy        419 TISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQ 478
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Db        336 RIYPSFTYYRSGEVLYLSCSADSNPPAQYSWTINEKFQLPGQKLFIRHITTKHSGLYVCS 395

Qy        479 ANNSASGHSRTTVKTITVSAELPKPSISSNN 509
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Db        396 VRNSATGKESSKSMTVEVSAYSSSINYTSGN 426


RESULT 14
B55181
pregnancy-specific beta-1-glycoprotein 11 form r precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C;Accession: B55181
R;McLenachan, P.A.; Rutherfurd, K.J.; Beggs, K.T.; Sims, S.E.; Mansfield, B.C.
Genomics 22, 356-363, 1994
A;Title: Characterization of the PSG11 gene.
A;Reference number: A55181; MUID:95104846; PMID:7806221
A;Accession: B55181
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-436 <MCL>
A;Cross-references: UNIPARC:UPI00001770AC; GB:U04324
C;Genetics:
A;Gene: GDB:PSG11
A;Cross-references: GDB:128242; OMIM:176398
A;Map position: 19q13.2-19q13.2
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: alternative splicing; glycoprotein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;255-312/Domain: immunoglobulin homology <IMM2>

  Query Match             30.4%;  Score 1130;  DB 2;  Length 436;
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  Matches  236;  Conservative   53;  Mismatches  126;  Indels   88;  Gaps    5;

Qy          6 APPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFGY 65
              ||     | |: |||||||| ||||||||::|||: |  |:|||:||||||||||:| ||
Db          6 APSCTQRITWKGLLLTASLLNFWNPPTTAEVTIEAQPPKVSEGKDVLLLVHNLPQNLPGY 65

Qy         66 SWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHVI 125
               |||||  |    || |::  :    |||||||| :| |||||||: : | | ||||:|
Db         66 FWYKGEMTDLYHYIISYIVDGKIIIYGPAYSGRETVYSNASLLIQNVTRKDAGTYTLHII 125

Qy        126 K-SDLVNEEATG-QFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQ 183
             | |   ||     | :| | ||| |||:|  | |  :||   |:||| ||:||||:| |
Db        126 KRGDETREEIRHFTFTLYLETPKPYISSSNLNPREAMEAVRLICDPETLDASYLWWMNGQ 185

Qy        184 SLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTIS 243
              ||||: |||||  |||| || ||:     |:|| :||||| ||| | ||:|
Db        186 SLPVTHRLQLSKTNRTLYLFGVTKYIAGPYECEIRNPVSASRSDPVTLNLL--------- 236

Qy        244 PLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHN 303
                                                                | :
Db        237 ----------------------------------------------PKL--------------- 239

Qy        304 SDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSL 363
                              | |:|| || || |::| :| |||: :| ||:||:| |||
Db        240 -------------------PIPYITINNLNPRENKDVLAFTCEPKSENYTYIWWLNGQSL 280

Qy        364 PVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISPS 423
              |||| ::   :|| | | |||||: |||:| |::       |:||||||||||| | | ||
Db        281 PVSPGVKRPIENRILILPSVTRNETGPYQCEIRDRYGGLRSNPVILNVLYGPDLPRIYPS 340

Qy        424 YTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSA 483
              :|||| | || |||   |||||:| | |:|  ||  |:|||  ||  :|||| |  :|||
Db        341 FTYYRSGENLDLSCFTESNPPAEYFWTINGKFQQSGQKLFIPQITRNHSGLYACSVHNSA 400

Qy        484 SGHSRTTVKTITVSAELPKPSIS 506
              :|   :   |: || |   | ::
Db        401 TGKEISKSMTVKVS-ETASPQVT 422


RESULT 15
A35964
pregnancy-specific glycoprotein I form d precursor - human
N;Alternate names: pregnancy-specific beta-1 glycoprotein 95; pregnancy-specific beta-
C;Species: Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 31-Oct-1997
C;Accession: A35964; B35964; B43354
R;Leslie, K.K.; Watanabe, S.; Lei, K.J.; Chou, D.Y.; Plouzek, C.A.; Deng, H.C.; Torres
Proc. Natl. Acad. Sci. U.S.A. 87, 5822-5826, 1990
A;Title: Linkage of two human pregnancy-specific beta-1-glycoprotein genes: one is ass
A;Reference number: A35964; MUID:90332674; PMID:2377620
A;Accession: A35964
A;Molecule type: mRNA
A;Residues: 1-426 <LES>
A;Cross-references: UNIPARC:UPI000017709E; GB:M34715
A;Accession: B35964
A;Molecule type: DNA
A;Residues: 237-426 <LE2>
A;Cross-references: UNIPARC:UPI000017709F; GB:M34716
R;Lei, K.J.; Sartwell, A.D.; Pan, C.J.; Chou, J.Y.
J. Biol. Chem. 267, 16371-16378, 1992
A;Title: Cloning and expression of genes encoding human pregnancy-specific glycoprotei
A;Reference number: A43354; MUID:92355602; PMID:1644821
A;Accession: B43354
A;Molecule type: DNA
A;Residues: 23-426 <LEI>
A;Cross-references: UNIPARC:UPI00001770A0
A;Note: sequence extracted from NCBI backbone (NCBIN:110710, NCBIN:110714, NCBIN:11071
C;Genetics:
A;Gene: GDB:PSG1
A;Cross-references: GDB:120321; OMIM:176390
A;Map position: 19q13.2-19q13.2
A;Introns: 122/1; 215/1; 308/1
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term
C;Keywords: glycoprotein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;162-219/Domain: immunoglobulin homology <IMM1>
F;255-312/Domain: immunoglobulin homology <IMM2>
F;347-396/Domain: immunoglobulin homology <IMM3>

  Query Match             30.3%;  Score 1127.5;  DB 2;  Length 426;
  Best Local Similarity   46.7%;  Pred. No. 3.7e-54;
  Matches  234;  Conservative   55;  Mismatches  125;  Indels   87;  Gaps    3;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              | : ||||    | |: |||||||| ||| ||||::|||: |  |:|||:||||||||||
Db          1 MGTLSAPPCTQRIKWKGLLLTASLLNFWNLPTTAQVTIEAEPTKVSEGKDVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :| || ||||:  |     |  ||:  :    ||||||||  | ||||||||: : | | |
Db         61 NLTGYIWYKGQMRDLYHYITSYVVDGEIIIYGPAYSGRETAYSNASLLIQNVTREDAGSY 120

Qy        121 TLHVIKSDLVNEEATGQ--FRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLW 178
              |||:|| |      ||:  | :: | |||||||:|  | |  :||: ||:||| ||:|||
Db        121 TLHIIKGDDGTRGVTGRFTFTLHLETPKPSISSSNLNPRETMEAVSLTCDPETPDASYLW 180

Qy        179 WVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPD 238
              |:| ||||::  |:||  |||| |  ||:     |:|| :||||| ||| | ||:|
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Db        181 WMNGQSLPMTHSLKLSETNRTLFLLGVTKYTAGPYECEIRNPVSASRSDPVTLNLL---- 236

Qy        239 APTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYT 298
                                                          | :
Db        237 ----------------------------------------------PKL--------- 239

Qy        299 CQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWV 358
                                  |||:|| || || |::| :  ||||: :| ||:||:
Db        240 ------------------------PKPYITINNLNPRENKDVLNFTCEPKSENYTYIWWL 275

Qy        359 NNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDP 418
              | |||||||||::   :|| | | |||||: |||:| |::      |||| |||||||| |
Db        276 NGQSLPVSPRVKRPIENRILILPSVTRNETGPYQCEIRDRYGGVRSDPVTLNVLYGPDLP 335

Qy        419 TISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQ 478
              | ||:|||| |  | ||| | ||||||||| |:   |   |:||| :|| |:|||| |
Db        336 RIYPSFTYYRSGEVLYLSCSADSNPPAQYSWTINEKFQLPGQKLFIRHITTKHSGLYVCS 395

Qy        479 ANNSASGHSRTTVKTITVSAE 499
              |||:|   :   |: || :
Db        396 VRNSATGKESSKSMTVEVSGK 416
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Search completed: April 10, 2006, 18:07:34
Job time : 42.1584 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:34 ; Search time 237.861 Seconds
(without alignments)
2082.225 Million cell updates/sec

Title: US-10-734-564-72
Perfect score: 3721
Sequence: 1 MESPSAPPHRWCIPWQRLLL.....LSAGATVGIMIGVLVGVALI 702

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3721	100.0	702	1	CEAM5_HUMAN	P06731 homo sapien
2	3717	99.9	702	2	Q8N4D0_HUMAN	Q8n4d0 homo sapien
3	3713	99.8	702	2	Q53G30_HUMAN	Q53g30 homo sapien
4	2066	55.5	420	2	Q68DM9_HUMAN	Q68dm9 homo sapien
5	1609	43.2	526	1	CEAM1_HUMAN	P13688 homo sapien
6	1600.5	43.0	464	2	Q16170_HUMAN	Q16170 homo sapien
7	1600.5	43.0	468	2	Q96CA7_HUMAN	Q96ca7 homo sapien
8	1526.5	41.0	525	2	Q5R9N6_PONPY	Q5r9n6 pongo pygma
9	1470	39.5	287	2	Q13984_HUMAN	Q13984 homo sapien
10	1443	38.8	344	1	CEAM6_HUMAN	P40199 homo sapien
11	1443	38.8	344	2	Q53XP7_HUMAN	Q53xp7 homo sapien
12	1443	38.8	344	2	Q13774_HUMAN	Q13774 homo sapien
13	1426.5	38.3	368	2	Q5UB49_HUMAN	Q5ub49 homo sapien
14	1423	38.2	461	2	Q13854_HUMAN	Q13854 homo sapien
15	1272	34.2	349	1	CEAM8_HUMAN	P31997 homo sapien
16	1194.5	32.1	373	2	Q7KYP5_HUMAN	Q7kyp5 homo sapien
17	1157.5	31.1	428	1	PSG3_HUMAN	Q16557 homo sapien
18	1148.5	30.9	419	1	PSG7_HUMAN	Q13046 homo sapien
19	1141.5	30.7	428	2	Q9BRW2_HUMAN	Q9brw2 homo sapien
20	1140.5	30.7	426	1	PSG8_HUMAN	Q9uq74 homo sapien
21	1134.5	30.5	419	2	Q68CR6_HUMAN	Q68cr6 homo sapien
22	1127.5	30.3	426	2	Q6ICR4_HUMAN	Q6icr4 homo sapien
23	1126.5	30.3	419	1	PSG1_HUMAN	P11464 homo sapien
24	1126.5	30.3	426	1	PSG9_HUMAN	Q00887 homo sapien
25	1125.5	30.2	426	2	Q6LEU7_HUMAN	Q6leu7 homo sapien
26	1124.5	30.2	411	2	Q15228_HUMAN	Q15228 homo sapien
27	1118.5	30.1	419	2	Q96QL5_HUMAN	Q96ql5 homo sapien
28	1117.5	30.0	419	2	Q6P520_HUMAN	Q6p520 homo sapien
29	1114.5	30.0	419	1	PSG4_HUMAN	Q00888 homo sapien
30	1107.5	29.8	435	1	PSG6_HUMAN	Q00889 homo sapien
31	1104	29.7	424	1	PSG10_HUMAN	Q15235 homo sapien
32	1070.5	28.8	521	2	Q61352_MOUSE	Q61352 mus musculu
33	1065.5	28.6	458	2	Q61351_MOUSE	Q61351 mus musculu
34	1023.5	27.5	521	1	CEAM1_MOUSE	P31809 mus musculu
35	1023.5	27.5	521	2	Q925P3_MOUSE	Q925p3 mus musculu
36	1018.5	27.4	454	2	Q91W54_MOUSE	Q91w54 mus musculu
37	998	26.8	520	2	Q925P2_MOUSE	Q925p2 mus musculu
38	992	26.7	459	2	Q9JHL6_RAT	Q9jhl6 rattus norv
39	983	26.4	458	2	Q63093_RAT	Q63093 rattus norv
40	980	26.3	448	2	Q9JHL7_RAT	Q9jhl7 rattus norv
41	970.5	26.1	519	1	CEAM1_RAT	P16573 rattus norv
42	919	24.7	402	2	Q15227_HUMAN	Q15227 homo sapien
43	901.5	24.2	352	2	Q15403_HUMAN	Q15403 homo sapien
44	900.5	24.2	352	2	Q08266_HUMAN	Q08266 homo sapien
45	898	24.1	332	1	PSG11_HUMAN	Q9uq72 homo sapien

ALIGNMENTS

RESULT 1
CEAM5_HUMAN
ID CEAM5_HUMAN STANDARD; PRT; 702 AA.
AC P06731;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinoembryonic antigen-related cell adhesion molecule 5 precursor
DE (Carcinoembryonic antigen) (CEA) (Meconium antigen 100) (CD66e
DE antigen).
GN Name=CEACAM5; Synonyms=CEA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90258861; PubMed=2342461;
RA Schrewe H., Thompson J., Bona M., Hefta L.J.F., Maruya A.,
RA Hassauer M., Shively J.E., von Kleist S., Zimmermann W.;
RT "Cloning of the complete gene for carcinoembryonic antigen: analysis
RT of its promoter indicates a region conveying cell type-specific
RT expression.";
RL Mol. Cell. Biol. 10:2738-2748(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88038876; PubMed=3670312;
RA Beauchemin N., Benchimol S., Cournoyer D., Fuks A., Stanners C.P.;
RT "Isolation and characterization of full-length functional cDNA clones
RT for human carcinoembryonic antigen.";
RL Mol. Cell. Biol. 7:3221-3230(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89122014; PubMed=3220478;
RA Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
RT "Carcinoembryonic antigen family: characterization of cDNAs coding for
RT NCA and CEA and suggestion of nonrandom sequence variation in their
RT conserved loop-domains.";
RL Genomics 3:59-66(1988).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 5-702.
RX MEDLINE=87128144; PubMed=3814146;
RA Oikawa S., Nakazato H., Kosaki G.;
RT "Primary structure of human carcinoembryonic antigen (CEA) deduced
RT from cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 142:511-518(1987).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 331-702.
RX MEDLINE=87204247; PubMed=3033671;
RA Zimmermann W., Ortlieb B., Friedrich R., von Kleist S.;
RT "Isolation and characterization of cDNA clones encoding the human
RT carcinoembryonic antigen reveal a highly conserved repeating
RT structure.";

```
RL   Proc. Natl. Acad. Sci. U.S.A. 84:2960-2964(1987).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: Found in adenocarcinomas of endodermally
CC       derived digestive system epithelium and fetal colon.
CC   -!- PTM: Complex immunoreactive glycoprotein with a MW of 180 kDa
CC       comprising 60% carbohydrate.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC   -!- SIMILARITY: Contains 7 Ig-like (immunoglobulin-like) domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M17303; AAB59513.1; -; Genomic_DNA.
DR   EMBL; M59262; AAA62835.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; M59255; AAA62835.1; JOINED; Genomic_DNA.
DR   EMBL; M59256; AAA62835.1; JOINED; Genomic_DNA.
DR   EMBL; M59257; AAA62835.1; JOINED; Genomic_DNA.
DR   EMBL; M59258; AAA62835.1; JOINED; Genomic_DNA.
DR   EMBL; M59259; AAA62835.1; JOINED; Genomic_DNA.
DR   EMBL; M59260; AAA62835.1; JOINED; Genomic_DNA.
DR   EMBL; M59261; AAA62835.1; JOINED; Genomic_DNA.
DR   EMBL; M59709; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR   EMBL; M59710; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR   EMBL; M29540; AAA51967.1; -; mRNA.
DR   EMBL; X16455; CAA34474.1; -; mRNA.
DR   EMBL; M15042; AAA51963.1; -; mRNA.
DR   EMBL; M16234; AAA51972.1; -; mRNA.
DR   PIR; A36319; A36319.
DR   PDB; 1E07; Model; A=35-676.
DR   Ensembl; ENSG00000105388; Homo sapiens.
DR   HGNC; HGNC:1817; CEACAM5.
DR   MIM; 114890; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 6.
DR   PROSITE; PS50835; IG_LIKE; 6.
KW   3D-structure; Glycoprotein; GPI-anchor; Immunoglobulin domain;
KW   Lipoprotein; Membrane; Repeat; Signal.
FT   SIGNAL        1     34
FT   CHAIN        35    685       Carcinoembryonic antigen-related cell
FT                                 adhesion molecule 5.
FT   PROPEP      686    702       Removed in mature form (Potential).
FT   DOMAIN       35    144       Ig-like 1.
FT   DOMAIN      146    237       Ig-like 2.
FT   DOMAIN      238    322       Ig-like 3.
FT   DOMAIN      324    415       Ig-like 4.
FT   DOMAIN      416    498       Ig-like 5.
FT   DOMAIN      502    593       Ig-like 6.
FT   DOMAIN      594    677       Ig-like 7.
FT   LIPID       685    685       GPI-anchor amidated alanine (Potential).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    115    115       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    152    152       N-linked (GlcNAc. . .) (Potential).
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FT   CARBOHYD    197    197       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    204    204       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    208    208       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    246    246       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    256    256       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    274    274       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    288    288       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    292    292       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    330    330       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    351    351       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    360    360       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    375    375       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    432    432       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    466    466       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    480    480       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    508    508       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    529    529       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    553    553       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    560    560       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    580    580       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    612    612       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    650    650       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    665    665       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    320    320       Missing (in Ref. 4).
SQ   SEQUENCE   702 AA;  76796 MW;  6299AE26CDDBDB5C CRC64;

  Query Match             100.0%;  Score 3721;  DB 1;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 6e-204;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 2
Q8N4D0_HUMAN
ID   Q8N4D0_HUMAN PRELIMINARY;      PRT;   702 AA.
AC   Q8N4D0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CEACAM5 protein.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR   EMBL; BC034671; AAH34671.1; -; mRNA.
DR   HSSP; Q61353; 1L6Z.
DR   Ensembl; ENSG00000105388; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 6.
DR   SMART; SM00408; IGc2; 3.
DR   PROSITE; PS50835; IG_LIKE; 6.
KW   Immunoglobulin domain; Transmembrane.
SQ   SEQUENCE   702 AA;  76782 MW;  97CCFB7399A0B05A CRC64;

  Query Match             99.9%;  Score 3717;  DB 2;  Length 702;
  Best Local Similarity   99.9%;  Pred. No. 1e-203;
  Matches  701;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDSASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 3
Q53G30_HUMAN
ID   Q53G30_HUMAN PRELIMINARY;      PRT;   702 AA.
AC   Q53G30;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 5 variant
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Maruyama K., Sugano S.;
RT   "Oligo-capping : a simple method to replace the cap structure of
RT   eucaryotic mRNAs with oligoribonucleotides.";
RL   Gene 138:171-174(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT   "Construction and characterization of a full length-enriched and a 5'-
RT   end-enriched cDNA library.";
RL   Gene 200:149-156(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA   Tanaka A., Yokoyama S.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK223101; BAD96821.1; -; mRNA.
FT   NON_TER       1       1
SQ   SEQUENCE   702 AA;  76867 MW;  62992426CDDABB5C CRC64;

  Query Match             99.8%;  Score 3713;  DB 2;  Length 702;
  Best Local Similarity   99.9%;  Pred. No. 1.7e-203;
  Matches  701;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
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Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDENIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 4
Q68DM9_HUMAN
ID   Q68DM9_HUMAN PRELIMINARY;      PRT;   420 AA.
AC   Q68DM9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein DKFZp781M2392.
GN   Name=DKFZp781M2392;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon carcinoma;
RG   The German cDNA Consortium;
RA   Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR749337; CAH18191.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   420 AA;  45508 MW;  6E30C0B4A00D0F59 CRC64;

  Query Match             55.5%;  Score 2066;  DB 2;  Length 420;
  Best Local Similarity   59.8%;  Pred. No. 7.5e-110;
  Matches  420;  Conservative    0;  Mismatches    0;  Indels  282;  Gaps    1;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNI-------- 112

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Db        113 ------------------------------------------------------------ 112

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Db        113 ------------------------------------------------------------ 112

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Db        113 ------------------------------------------------------------ 112

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Db        113 ------------------------------------------------------------ 112

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
                                                ||||||||||||||||||||||||
Db        113 ---------------------------------IQNELSVDHSDPVILNVLYGPDDPTI 138

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 198

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 258

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 318

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 378

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        379 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 420


RESULT 5
CEAM1_HUMAN
ID   CEAM1_HUMAN    STANDARD;      PRT;   526 AA.
AC   P13688; O60430; Q13858; Q15600; Q9UQV9;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 1 precursor
DE   (Biliary glycoprotein 1) (BGP-1) (Antigen CD66) (CD66a antigen).
GN   Name=CEACAM1; Synonyms=BGP, BGP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM A), AND PARTIAL PROTEIN SEQUENCE.
RX   MEDLINE=88320555; PubMed=2457922;
RA   Hinoda Y., Neumaier M., Hefta S.A., Drzeniek Z., Wagener C.,
RA   Shively L., Hefta L.J.F., Shively J.E., Paxton R.J.;
RT   "Molecular cloning of a cDNA coding biliary glycoprotein I: primary
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RT   structure of a glycoprotein immunologically crossreactive with
RT   carcinoembryonic antigen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:6959-6963(1988).
RN   [2]
RP   ERRATUM, AND SEQUENCE REVISION.
RA   Hinoda Y., Neumaier M., Hefta S.A., Drzeniek Z., Wagener C.,
RA   Shively L., Hefta L.J.F., Shively J.E., Paxton R.J.;
RL   Proc. Natl. Acad. Sci. U.S.A. 86:1668-1668(1989).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS A AND B).
RX   MEDLINE=89139550; PubMed=2537311; DOI=10.1083/jcb.108.2.267;
RA   Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA   Elting J.J., Kamarck M.E.;
RT   "Carcinoembryonic antigens: alternative splicing accounts for the
RT   multiple mRNAs that code for novel members of the carcinoembryonic
RT   antigen family.";
RL   J. Cell Biol. 108:267-276(1989).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS A; B; C; G; H AND I).
RC   TISSUE=Leukocyte;
RX   MEDLINE=91222218; PubMed=2025273;
RA   Kuroki M., Arakawa F., Matsuo Y., Oikawa S., Nakazato H., Matsuoka Y.;
RT   "Three novel molecular forms of biliary glycoprotein deduced from cDNA
RT   clones from a human leukocyte library.";
RL   Biochem. Biophys. Res. Commun. 176:578-585(1991).
RN   [5]
RP   NUCLEOTIDE SEQUENCE (ISOFORM D).
RX   MEDLINE=93140765; PubMed=8423792;
RA   Barnett T.R., Drake L., Pickle W. II;
RT   "Human biliary glycoprotein gene: characterization of a family of
RT   novel alternatively spliced RNAs and their expressed proteins.";
RL   Mol. Cell. Biol. 13:1273-1282(1993).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15057824; DOI=10.1038/nature02399;
RA   Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA   Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA   Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA   Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA   Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
RA   Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA   Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA   Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA   Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA   Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA   Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA   Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
RA   Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA   Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA   Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA   Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA   Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA   Rubin E.M., Lucas S.M.;
RT   "The DNA sequence and biology of human chromosome 19.";
RL   Nature 428:529-535(2004).
RN   [7]
RP   NUCLEOTIDE SEQUENCE OF 1-21, AND DISEASE.
RX   MEDLINE=94333343; PubMed=8055923;
RA   Hauck W., Nedellec P., Turbide C., Stanners C.P., Barnett T.R.,
RA   Beauchemin N.;
RT   "Transcriptional control of the human biliary glycoprotein gene, a CEA
RT   gene family member down-regulated in colorectal carcinomas.";
RL   Eur. J. Biochem. 223:529-541(1994).
RN   [8]
RP   NUCLEOTIDE SEQUENCE OF 1-21.
RX   MEDLINE=95354678; PubMed=7628460;
RA   Nedellec P., Turbide C., Beauchemin N.;
RT   "Characterization and transcriptional activity of the mouse biliary
RT   glycoprotein 1 gene, a carcinoembryonic antigen-related gene.";
RL   Eur. J. Biochem. 231:104-114(1995).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform A, isoform
CC       B and isoform C). Secreted (isoform G, isoform H and isoform I).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=7;
CC       Name=A;
CC         IsoId=P13688-1; Sequence=Displayed;
CC       Name=G;
CC         IsoId=P13688-2; Sequence=VSP_002482, VSP_002483;
CC       Name=H;
CC         IsoId=P13688-3; Sequence=VSP_002478, VSP_002479;
CC       Name=I;
CC         IsoId=P13688-4; Sequence=VSP_002480, VSP_002481;
CC       Name=B;
CC         IsoId=P13688-5; Sequence=VSP_009227;
CC       Name=C;
CC         IsoId=P13688-6; Sequence=VSP_010938;
CC       Name=D;
CC         IsoId=P13688-7; Sequence=VSP_012222;
CC   -!- DISEASE: Loss or reduced expression is a major event in colorectal
CC       carcinogenesis.
CC   -!- DISEASE: Increased serum levels of BGP-1 are found in individuals
CC       suffering from hepatic disorders.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC   -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC       domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; J03858; AAA51826.1; -; mRNA.
DR   EMBL; X16354; CAA34404.1; -; mRNA.
DR   EMBL; D90311; BAA14341.1; -; mRNA.
DR   EMBL; D90312; BAA14342.1; -; mRNA.
DR   EMBL; D90313; BAA14343.1; -; mRNA.
DR   EMBL; X14831; CAA32940.1; -; mRNA.
DR   EMBL; M69176; AAA51825.1; -; mRNA.
DR   EMBL; M72238; AAA58393.1; -; mRNA.
DR   EMBL; M72238; AAA58394.1; -; mRNA.
DR   EMBL; M76742; AAA57142.1; -; mRNA.
DR   EMBL; AC004785; AAC18433.1; -; Genomic_DNA.
DR   EMBL; AC004785; AAC18434.1; -; Genomic_DNA.
DR   EMBL; AC004785; AAC18435.1; -; Genomic_DNA.
DR   EMBL; AC004785; AAC18437.1; -; Genomic_DNA.
DR   EMBL; AC004785; AAC18438.1; -; Genomic_DNA.
DR   EMBL; AC004785; AAC18439.1; -; Genomic_DNA.
DR   EMBL; X67277; CAA47694.1; -; Genomic_DNA.
DR   PIR; A32164; A32164.
DR   PIR; JH0394; JH0394.
DR   PIR; JH0395; JH0395.
DR   PIR; JH0396; JH0396.
DR   HSSP; Q61353; 1L6Z.
DR   Ensembl; ENSG00000079385; Homo sapiens.
DR   HGNC; HGNC:1814; CEACAM1.
DR   MIM; 109770; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0001525; P:angiogenesis; NAS.
DR   GO; GO:0016477; P:cell migration; NAS.
DR   GO; GO:0007156; P:homophilic cell adhesion; NAS.
DR   GO; GO:0007229; P:integrin-mediated signaling pathway; NAS.
DR   GO; GO:0007565; P:pregnancy; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin domain; Pyrrolidone carboxylic acid; Repeat; Signal;
KW   Transmembrane.
FT   SIGNAL       1     34
FT   CHAIN       35    526       Carcinoembryonic antigen-related cell
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FT                                adhesion molecule 1.
FT   TOPO_DOM     35    428       Extracellular (Potential).
FT   TRANSMEM    429    452       Potential.
FT   TOPO_DOM    453    526       Cytoplasmic (Potential).
FT   DOMAIN       35    142       Ig-like V-type.
FT   DOMAIN      145    232       Ig-like C2-type 1.
FT   DOMAIN      237    317       Ig-like C2-type 2.
FT   DOMAIN      323    413       Ig-like C2-type 3.
FT   MOD_RES      35     35       Pyrrolidone carboxylic acid.
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .).
FT   CARBOHYD    111    111       N-linked (GlcNAc. . .).
FT   CARBOHYD    115    115       N-linked (GlcNAc. . .).
FT   CARBOHYD    152    152       N-linked (GlcNAc. . .).
FT   CARBOHYD    182    182       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    197    197       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    208    208       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    224    224       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    232    232       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    254    254       N-linked (GlcNAc. . .).
FT   CARBOHYD    274    274       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    288    288       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    292    292       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    302    302       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    345    345       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    351    351       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    363    363       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    378    378       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    405    405       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    167    215       Probable.
FT   DISULFID    259    299       Probable.
FT   DISULFID    348    396       Probable.
FT   VARSPLIC    143    416       Missing (in isoform D).
FT                                /FTId=VSP_012222.
FT   VARSPLIC    320    416       ELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWF

  Query Match           43.2%;  Score 1609;  DB 1;  Length 526;
  Best Local Similarity   62.7%;  Pred. No. 1.1e-83;
  Matches  326;  Conservative   47;  Mismatches  121;  Indels   26;  Gaps    6;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||||:|| || ||||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |||||||||||||||:|| |||||||||||  |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||||| ||||||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
               :| || | ||:|||:|||||||||||| :|||||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
               || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
              ||| | |::||  | ||::  | | | | | | : | :| : |||::||| |   | :
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDG---------NIQQHTQELFISNITEK 470
              :||       |: : :    |    |   :|  |         :: :|     :|| |:
Db        425 LSPGAI---AGIVIGVVALVALIAVALACFLHFGKTGRASDQRDLTEHKPS--VSNHTQD 479

Qy        471 NSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNS 510
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              :|       |: :  :  |  |:   |: |    |:: |
Db        480 HS-------NDPPNKMNEVTYSTLNFEAQQPTQPTSASPS 512


RESULT 6
Q16170_HUMAN
ID   Q16170_HUMAN PRELIMINARY;      PRT;   464 AA.
AC   Q16170; Q15601;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   BGPc (BGPc_HUMAN).
GN   Name=BGPc; Synonyms=BGP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94289702; PubMed=8018919;
RA   Watt S.M., Fawcett J., Murdoch S.J., Teixeira A.M., Gschmeissner S.E.,
RA   Hajibagheri N.M., Simmons D.L.;
RT   "CD66 identifies the biliary glycoprotein (BGP) adhesion molecule:
RT   cloning, expression, and adhesion functions of the BGPc splice
RT   variant.";
RL   Blood 84:200-210(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA   Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA   Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA   Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA   Kobayashi A., Olsen A.S., Carrano A.V.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR   EMBL; S71326; AAB31183.1; -; mRNA.
DR   EMBL; AC004785; AAC18436.1; -; Genomic_DNA.
DR   PIR; C30127; C30127.
DR   HSSP; Q61353; 1L6Z.
DR   Ensembl; ENSG00000079385; Homo sapiens.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   464 AA;  50521 MW;  598E4D71BF05EDA9 CRC64;

  Query Match           43.0%;  Score 1600.5;  DB 2;  Length 464;
  Best Local Similarity   73.0%;  Pred. No. 3e-83;
  Matches  309;  Conservative   30;  Mismatches   79;  Indels    5;  Gaps    2;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| || ||||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |||||||||||||||:|| |||||||||||  |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||||| ||||||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244
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Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
              :| || | ||:|||:|||||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
               || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
              ||| | |::||  | ||::  | | | | | | : | :| : |||::||| |   | :
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISP 422
              :||
Db        425 LSP 427
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RESULT 7
Q96CA7_HUMAN
ID Q96CA7_HUMAN PRELIMINARY; PRT; 468 AA.
AC Q96CA7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CEACAM1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; BC014473; AAH14473.1; -; mRNA.
DR HSSP; Q61353; 1L6Z.
DR Ensembl; ENSG00000079385; Homo sapiens.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 468 AA; 51147 MW; 215C1A33EEFFFD68 CRC64;

Query Match 43.0%; Score 1600.5; DB 2; Length 468;
Best Local Similarity 73.0%; Pred. No. 3e-83;
Matches 309; Conservative 30; Mismatches 79; Indels 5; Gaps 2;

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Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| || |||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |||||||||||||||:|| |||||||||| |||| ||||||||||: |||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
              :| || | ||:|||:|||||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
               || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
              ||| | |::||  | ||::  | | | | | | : | :| : |||::||| |   | :
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISP 422
              :||
Db        425 LSP 427
```

RESULT 8
Q5R9N6_PONPY
ID Q5R9N6_PONPY PRELIMINARY; PRT; 525 AA.
AC Q5R9N6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469J1620.
GN Name=DKFZp469J1620;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CR859350; CAH91524.1; -; mRNA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGc2; 3.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 525 AA; 57728 MW; 32BED1597026EEA3 CRC64;

Query Match 41.0%; Score 1526.5; DB 2; Length 525;

```
  Best Local Similarity   58.8%;  Pred. No. 5.7e-79;
  Matches  310;  Conservative   51;  Mismatches  125;  Indels   41;  Gaps    6;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| |||||||||||||||||||:  |
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESTPFNVAEGKEVLLLVHNLPQNPLG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |:||||| || | :|||||   |  |||||| || ||||||||||: |||||||| |
Db         65 YNWYKGEMVDANHRIIGYVISDQLTTPGPAYSSREKIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||| ||| |||||| |||| |||| |||| ||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPETPKPFISSNNSNPVEDNDAVALTCEPGTQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              ||:|||||||||||||| :|||||    |:|| |||||| ||| | ||| |||| |||||
Db        185 LPISPRLQLSNGNRTLTLLSVTRNDAGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
               :| || | ||:|||:|||||||||| :|||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP--KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQS 362
              || ||||| || |    |  || | :: :   ||:|:| |||      :  |:  |||
Db        305 VTGRNRTTVKTIIVTELSPVVKPQIKASKTTVTEDKDSVNLTCSTNDTGISISWFFENQS 364

Qy        363 LPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISP 422
              || | |::||  | ||::  | | | | | : | :| : |||::|:| | |
Db        365 LPSSERMKLSQGNTTLSINPVKREDAGKYWCEVFNSISKNQSDPIMLSVKY--------- 415

Qy        423 SYTYYRPGVN------------------LSLSCHAASNPPAQYSWLIDGNIQQHTQELF 463
              :|     |::                  ::|:|       : |   |  : :|
Db        416 NYPSQENGLSAGAIAGIVIGVLALVALIAVALACFLHFRKTGRASDQRD--LTEHKPS-- 471

Qy        464 ISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNS 510
              :|| |: :|      |:  :  :  |  |:   |: |  | |:: |
Db        472 VSNHTQDHS-------NDPPNKMNEVTYSTLNFEAQQPTQSTSASPS 511


RESULT 9
Q13984_HUMAN
ID   Q13984_HUMAN PRELIMINARY;      PRT;   287 AA.
AC   Q13984;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CEA protein (Fragment).
GN   Name=CEA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87260984; PubMed=2955415;
RA   Kamarck M.E., Elting J.J., Hart J.T., Goebel S.J., Rae P.M.,
RA   Nothdurft M.A., Nedwin J.J., Barnett T.R.;
RT   "Carcinoembryonic antigen family: expression in a mouse L-cell
RT   transfectant and characterization of a partial cDNA in bacteriophage
RT   lambda gt11.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:5350-5354(1987).
DR   EMBL; M17191; AAA51968.1; -; mRNA.
DR   PIR; A28333; A28333.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
FT   NON_TER       1      1
FT   NON_TER     287    287
SQ   SEQUENCE   287 AA;  31553 MW;  70BD1CF30FEE1166 CRC64;


  Query Match             39.5%;  Score 1470;  DB 2;  Length 287;
  Best Local Similarity   98.6%;  Pred. No. 4.5e-76;
  Matches  276;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        322 PPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLL 381
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 PIKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLL 66

Qy        382 SVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAAS 441
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 SVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAAS 126

Qy        442 NPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELP 501
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||::|
Db        127 NPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSASGHSRTTVKTITVSADVP 186

Qy        502 KPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNV 561
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        187 KPSISSNNSKPVEDKDAVAFHCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNV 246

Qy        562 TRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPP 601
              |||||||||||||||||||||||||||||||||||||||||
Db        247 TRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPP 286


RESULT 10
CEAM6_HUMAN
ID   CEAM6_HUMAN    STANDARD;      PRT;   344 AA.
AC   P40199; Q14920;
DT   01-FEB-1995 (Rel. 31, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 6 precursor
DE   (Normal cross-reacting antigen) (Nonspecific crossreacting antigen)
DE   (CD66c antigen).
GN   Name=CEACAM6; Synonyms=NCA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89122014; PubMed=3220478;
RA   Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
RT   "Carcinoembryonic antigen family: characterization of cDNAs coding for
RT   NCA and CEA and suggestion of nonrandom sequence variation in their
RT   conserved loop-domains.";
RL   Genomics 3:59-66(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=88106638; PubMed=3337731;
RA   Tawaragi Y., Oikawa S., Matsuoka Y., Kosaki G., Nakazato H.;
RT   "Primary structure of nonspecific crossreacting antigen (NCA), a
RT   member of carcinoembryonic antigen (CEA) gene family, deduced from
RT   cDNA sequence.";
RL   Biochem. Biophys. Res. Commun. 150:89-96(1988).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   PROTEIN SEQUENCE OF 35-49.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC   -!- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC       domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M29541; AAA59915.1; -; mRNA.
DR   EMBL; M18728; AAA59907.1; -; mRNA.
DR   EMBL; BC005008; AAH05008.1; -; mRNA.
DR   HSSP; Q61353; 1L6Z.
DR   Ensembl; ENSG00000086548; Homo sapiens.
DR   HGNC; HGNC:1818; CEACAM6.
DR   H-InvDB; HIX0015160; -.
DR   MIM; 163980; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Antigen; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW   Immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT   SIGNAL        1     34
FT   CHAIN        35    320       Carcinoembryonic antigen-related cell
FT                                 adhesion molecule 6.
FT   PROPEP      321    344       Removed in mature form (By similarity).
FT   DOMAIN       35    142       Ig-like V-type.
FT   DOMAIN      145    232       Ig-like C2-type 1.
FT   DOMAIN      237    314       Ig-like C2-type 2.
FT   LIPID       320    320       GPI-anchor amidated glycine (By
FT                                 similarity).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    111    111       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    115    115       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    152    152       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    173    173       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    197    197       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    224    224       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    256    256       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    274    274       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    288    288       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    292    292       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    167    215       Probable.
FT   DISULFID    259    299       Probable.
FT   CONFLICT    138    138       F -> L (in Ref. 1).
FT   CONFLICT    239    239       V -> G (in Ref. 1).
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SQ   SEQUENCE   344 AA;  37237 MW;  4322C5D6E25849F5 CRC64;

  Query Match             38.8%;  Score 1443;  DB 1;  Length 344;
  Best Local Similarity   83.9%;  Pred. No. 1.9e-74;
  Matches  271;  Conservative   11;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |  ||||| |  :||: :||||||||||||||||||||||||||||||||||||||||| |||||
Db          1 MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  |||||||||||||  |:||||||||||||||||||| ||||||||||: |||||||
Db         61 NRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              || |||||||||||||||  |||||||||||||||  |||||||||||||||  |: ||||||
Db        121 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              | ||||||||||||||| |||| :| |||  ||:|| ||| || ||| | ||||||| |
Db        181 NGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDVP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||   :|| ||||||||||||||||||:|||||||||||||||||||||||||| ||
Db        241 TISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFQQSTQELFIPNITVNNSGSYMCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPP 323
              |||| ||||||||| |||    |
Db        301 AHNSATGLNRTTVTMITVSGSAP 323


RESULT 11
Q53XP7_HUMAN
ID   Q53XP7_HUMAN PRELIMINARY;      PRT;   344 AA.
AC   Q53XP7;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 6 (Non-
DE   specific cross reacting antigen).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT009774; AAP88776.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   344 AA;  37237 MW;  4322C5D6E25849F5 CRC64;

  Query Match             38.8%;  Score 1443;  DB 2;  Length 344;
  Best Local Similarity   83.9%;  Pred. No. 1.9e-74;
  Matches  271;  Conservative   11;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |  ||||| |  :||: :||||||||||||||||||||||||||||||||||||||||| |||||
Db          1 MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  |||||||||||||  |:||||||||||||||||||| ||||||||||: |||||||
Db         61 NRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFY 120
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Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              || |||||||||||||| |||||||||||||| |||||||||||||| |: ||||||
Db        121 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              | |||||||||||||| |||| :| |||  ||:|| ||| || ||| | ||||||| |
Db        181 NGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDVP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||   :|| |||||||||||||||||:|||||||||||||||||||||||||||| ||
Db        241 TISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFQQSTQELFIPNITVNNSGSYMCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPP 323
              |||| ||||||||| |||    |
Db        301 AHNSATGLNRTTVTMITVSGSAP 323


RESULT 12
Q13774_HUMAN
ID   Q13774_HUMAN PRELIMINARY;      PRT;   344 AA.
AC   Q13774;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   NCA protein precursor.
GN   Name=NCA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88139389; PubMed=2830274;
RA   Neumaier M., Zimmermann W., Shively L., Hinoda Y., Riggs A.D.,
RA   Shively J.E.;
RT   "Characterization of a cDNA clone for the nonspecific cross-reacting
RT   antigen (NCA) and a comparison of NCA and carcinoembryonic antigen.";
RL   J. Biol. Chem. 263:3202-3207(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87298464; PubMed=3619891;
RA   Oikawa S., Kosaki G., Nakazato H.;
RT   "Molecular cloning of a gene for a member of carcinoembryonic antigen
RT   (CEA) gene family; signal peptide and N-terminal domain sequences of
RT   nonspecific crossreacting antigen (NCA).";
RL   Biochem. Biophys. Res. Commun. 146:464-469(1987).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR   EMBL; M18216; AAA51739.1; -; mRNA.
DR   PIR; A26902; A27681.
DR   HSSP; Q61353; 1L6Z.
DR   Ensembl; ENSG00000086548; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Signal; Transmembrane.
FT   SIGNAL        1     34       Potential.
FT   CHAIN        35    344       Potential.
SQ   SEQUENCE   344 AA;  37195 MW;  28469487A74C18A4 CRC64;

  Query Match             38.8%;  Score 1443;  DB 2;  Length 344;
  Best Local Similarity   83.9%;  Pred. No. 1.9e-74;
  Matches  271;  Conservative   11;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |  ||||| |  :||: :||||||||||||||||||||||||||||||||||||| |||||
Db          1 MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  |||||||||||||  |:||||||||||||||||||| ||||||||||: |||||||
Db         61 NRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              || |||||||||||||| |||||||||||||| |||||||||||||| |: ||||||
Db        121 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              | |||||||||||||| |||| :| |||  ||:|| ||| || ||| | ||||||| |
Db        181 NGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||   :|| |||||||||||||||||:|||||||||||||||||||||||||||| ||
Db        241 TISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFQQSTQELFIPNITVNNSGSYMCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPP 323
              |||| ||||||||| |||    |
Db        301 AHNSATGLNRTTVTMITVSGSAP 323


RESULT 13
Q5UB49_HUMAN
ID   Q5UB49_HUMAN PRELIMINARY;      PRT;   368 AA.
AC   Q5UB49;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Putative carcinoembryonic antigen-related cell adhesion molecule 1
DE   short form 3.
GN   Name=CEACAM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Long S., Phillips A., Ma H., Paoni N.F., Wong-Staal F., Fan W.;
RT   "Isolation of the cDNA encoding a putative carcinoembryonic antigen-
RT   related cell adhesion molecule 1 short form 3 (CEACAM1-3S).";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY766113; AAV34600.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000920; Myelin_P0.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR00213; MYELINP0.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   368 AA;  39871 MW;  23D7E54B4DC54318 CRC64;

  Query Match             38.3%;  Score 1426.5;  DB 2;  Length 368;
  Best Local Similarity   76.7%;  Pred. No. 1.8e-73;
  Matches  276;  Conservative   16;  Mismatches   39;  Indels   29;  Gaps    2;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| || |||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |||||||||||||:|| |||||||||| |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
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                ||||||||||||||||||| :||||||  |:|| ||||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
                :| || | ||:|||:|||||||||| :|||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDE-------------------DAVALTC 345
                || ||||| ||           | ::|: | |:                    |||| |
Db        305 VTGCNRTTVKTI----------IVTDNALPQENGLSPGAIAGIVIGVVALVALIAVALAC 354


RESULT 14
Q13854_HUMAN
ID   Q13854_HUMAN PRELIMINARY;      PRT;   461 AA.
AC   Q13854;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Biliary glycoprotein.
GN   Name=BGP;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89139550; PubMed=2537311; DOI=10.1083/jcb.108.2.267;
RA   Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA   Elting J.J., Kamarck M.E.;
RT   "Carcinoembryonic antigens: alternative splicing accounts for the
RT   multiple mRNAs that code for novel members of the carcinoembryonic
RT   antigen family.";
RL   J. Cell Biol. 108:267-276(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Kuroki M., Matsuo Y., Misumi Y., Oikawa S., Matsuoka Y.;
RL   Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR   EMBL; D12502; BAA02063.1; -; mRNA.
DR   HSSP; Q61353; 1L6Z.
DR   Ensembl; ENSG00000079385; Homo sapiens.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   461 AA;  50298 MW;  4A6F0F05884C4727 CRC64;

  Query Match             38.2%;  Score 1423;  DB 2;  Length 461;
  Best Local Similarity   63.0%;  Pred. No. 3.9e-73;
  Matches  298;  Conservative   27;  Mismatches   68;  Indels   80;  Gaps   10;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| || |||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |||||||||||||:|| |||||||||| |||| ||||||||||: |||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
                | || | ||:|||:|||||||||| :|||||||||||||||||||||||| |:||
Db        245 SYTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITV----------------YAEPPKPFIT-----SNNSNPVEDE----- 338
                || ||||| || |                :|:   | ::     ::|: | |:
Db        305 VTGCNRTTVKTIIVTERQNLTMLPGLDSNSWAQAILPSVSQSAEITDNALPQENGLSPGA 364

Qy        339 --------------DAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVT 384
                           |||| |      |                    ::| | ||
Db        365 IAGIVIGVVALVALIAVALACFLHFGKT-----------------GRASDQRDLT----- 402

Qy        385 RNDVGPYECGIQNELSVDHSD--PVILN-VLYG--------PDDPT-ISPSYT 425
                  ::  : |  : |||:  |  :| | |          |  ||  ||| |
Db        403 -----EHKPSVSNH-TQDHSNDPPNKMNEVTYSTLNFEAQQPTQPTSASPSLT 449


RESULT 15
CEAM8_HUMAN
ID   CEAM8_HUMAN    STANDARD;      PRT;   349 AA.
AC   P31997; O60399; Q16574;
DT   01-JUL-1993 (Rel. 26, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 8 precursor
DE   (Carcinoembryonic antigen CGM6) (Nonspecific cross-reacting antigen
DE   NCA-95) (Antigen CD67) (CD66b antigen).
GN   Name=CEACAM8; Synonyms=CGM6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=91003998; PubMed=2208113;
RA   Berling B., Kolbinger F., Grunert F., Thompson J.A., Brombacher F.,
RA   Buchegger F., Vkleist S., Zimmermann W.;
RT   "Cloning of a carcinoembryonic antigen gene family member expressed in
RT   leukocytes of chronic myeloid leukemia patients and bone marrow.";
RL   Cancer Res. 50:6534-6539(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90165902; PubMed=2306228;
RA   Arakawa F., Kuroki M., Misumi Y., Oikawa S., Nakazato H., Matsuoka Y.;
RT   "Characterization of a cDNA clone encoding a new species of the
RT   nonspecific cross-reacting antigen (NCA), a member of the CEA gene
RT   family.";
RL   Biochem. Biophys. Res. Commun. 166:1063-1071(1990).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1427854;
RA   Khan W.N., Fraengsmyr L., Teglund S., Israelsson A., Bremer K.,
RA   Hammarstroem S.;
RT   "Identification of three new genes and estimation of the size of the
RT   carcinoembryonic antigen family.";
RL   Genomics 14:384-390(1992).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15057824; DOI=10.1038/nature02399;
RA   Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA   Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA   Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA   Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA   Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
RA   Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA   Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA   Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA   Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA   Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA   Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA   Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
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RA   Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA   Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA   Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA   Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA   Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA   Rubin E.M., Lucas S.M.;
RT   "The DNA sequence and biology of human chromosome 19.";
RL   Nature 428:529-535(2004).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 1-21.
RX   MEDLINE=98102450; PubMed=9427723;
RA   Eades-Perner A., Thompson J., van der Putten H., Zimmermann W.;
RT   "Mice transgenic for the human CGM6 gene express its product, the
RT   granulocyte marker CD66b, exclusively in granulocytes.";
RL   Blood 91:663-672(1998).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: Expressed in leukocytes of chronic myeloid
CC       Leukemia patients and bone marrow.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC   -!- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC       domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X52378; CAA36604.1; -; mRNA.
DR   EMBL; M33326; AAA59914.1; -; mRNA.
DR   EMBL; D90064; BAA14108.1; -; mRNA.
DR   EMBL; AC004558; AAC13659.1; -; Genomic_DNA.
DR   EMBL; BC026263; AAH26263.1; -; mRNA.
DR   EMBL; Z95119; CAB08298.1; -; Genomic_DNA.
DR   PIR; S13524; A34815.
DR   HSSP; Q61353; 1L6Z.
DR   Ensembl; ENSG00000124469; Homo sapiens.
DR   HGNC; HGNC:1820; CEACAM8.
DR   H-InvDB; HIX0018406; -.
DR   MIM; 114890; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 3.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Antigen; Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;
KW   Membrane; Polymorphism; Repeat; Signal.
FT   SIGNAL        1     34
FT   CHAIN        35    320       Carcinoembryonic antigen-related cell
FT                                 adhesion molecule 8.
FT   PROPEP      321    349       Removed in mature form.
FT   DOMAIN       35    142       Ig-like V-type.
FT   DOMAIN      145    232       Ig-like C2-type 1.
FT   DOMAIN      237    319       Ig-like C2-type 2.
FT   LIPID       320    320       GPI-anchor amidated aspartate.
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    111    111       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    115    115       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    152    152       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    173    173       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    197    197       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    224    224       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    256    256       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    274    274       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    288    288       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    167    215       Probable.
FT   DISULFID    259    299       Probable.
FT   VARIANT     114    114       R -> K (in dbSNP:1041997).
FT                                 /FTId=VAR_011721.
FT   CONFLICT    322    322       L -> V (in Ref. 2).
SQ   SEQUENCE   349 AA;  38154 MW;  AACF74DA1AC839D8 CRC64;

  Query Match             34.2%;  Score 1272;  DB 1;  Length 349;
  Best Local Similarity   76.8%;  Pred. No. 1.1e-64;
  Matches  241;  Conservative   19;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              |||  || |||| ||||||| |||||||||:||||: | | ||||||||||||||    |
Db          5 SAPSCRWRIPWQGLLLTASLFTFWNPPTTAQLTIEAVPSNAAEGKEVLLLVHNLPQDPRG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              |:||||| || ||:||||||  || ||||||| || ||||||||::|: :|||| ||| |
Db         65 YNWYKGETVDANRRIIGYVISNQQITPGPAYSNRETIYPNASLLMRNVTRNDTGSYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              || :|::|| |||| |:|| |||||||||| ||||||||||||||||: ||||||| ||
Db        125 IKLNLMSEEVTGQFSVHPETPKPSISSNNSNPVEDKDAVAFTCEPETQNTTYLWWVNGQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||||| :|||||   |:|| ||| ||  || | ||||||||||||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDVGPYECEIQNPASANFSDPVTLNVLYGPDAPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
              :| | :| |||||||||||||:|||| ||||||| ||:|||||||  ||||| |    ||
Db        245 SDTYYHAGVNLNLSCHAASNPPSQYSWSVNGTFQQYTQKLFIPNITTKNSGSYACHTTNS 304

Qy        305 DTGLNRTTVTTITV 318
              || |||||  |||
Db        305 ATGRNRTTVRMITV 318


Search completed: April 10, 2006, 18:06:36
Job time : 239.861 secs
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Goddard, L.
10173456 4
Seq. IDS 72 # 100

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:05 ; Search time 270.297 Seconds
(without alignments)
1141.129 Million cell updates/sec

Title: US-10-734-564-72
Perfect score: 3721
Sequence: 1 MESPSAPPHRWCIPWQRLLL.....LSAGATVGIMIGVLVGVALI 702

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3721	100.0	702	5	ABB75931	Abb75931 Carcinoem
2	3721	100.0	702	6	ABU56667	Abu56667 Lung canc
3	3721	100.0	702	6	ABU56426	Abu56426 Lung canc
4	3721	100.0	702	6	ADA84059	Ada84059 Human CEA
5	3721	100.0	702	6	ABP74707	Abp74707 Human CEA
6	3721	100.0	702	6	ABU04837	Abu04837 Human exp
7	3721	100.0	702	6	ABU04800	Abu04800 Human exp
8	3721	100.0	702	6	ABU04834	Abu04834 Human exp
9	3721	100.0	702	6	ABU04796	Abu04796 Human exp
10	3721	100.0	702	7	ABR82476	Abr82476 Human car
11	3721	100.0	702	7	ADC09591	Adc09591 CEA prote
12	3721	100.0	702	7	ADD25526	Add25526 Binding d
13	3721	100.0	702	7	ADD46175	Add46175 Human Pro
14	3721	100.0	702	7	ADD84721	Add84721 Human car
15	3721	100.0	702	7	ADN39014	Adn39014 Cancer/an
16	3721	100.0	702	8	ADM72829	Adm72829 Human CEA
17	3721	100.0	702	8	ADO49153	Ado49153 Human car
18	3721	100.0	702	8	ADO28645	Ado28645 Human CEA
19	3721	100.0	702	8	ADQ29646	Adq29646 Human col
20	3721	100.0	702	8	ADP80107	Adp80107 Human epi
21	3721	100.0	702	8	ADT50889	Adt50889 Cancer re
22	3721	100.0	702	8	ADT77676	Adt77676 Human car
23	3721	100.0	702	8	ADU06621	Adu06621 Novel bro
24	3721	100.0	702	8	ADU73922	Adu73922 Human car
25	3721	100.0	702	9	ADV73224	Adv73224 Human col
26	3721	100.0	702	9	ADV73228	Adv73228 Human col
27	3721	100.0	702	9	AEB29747	Aeb29747 Human car
28	3721	100.0	708	8	ADR89125	Adr89125 Human car
29	3721	100.0	734	2	AAW00182	Aaw00182 Carcinoem
30	3721	100.0	734	6	ABU04823	Abu04823 Human exp
31	3718	99.9	796	4	AAB70880	Aab70880 Human car
32	3718	99.9	796	6	ABU04812	Abu04812 Human exp
33	3714	99.8	702	8	ADO38542	Ado38542 Carcinoem
34	3713	99.8	702	8	ADM12322	Adm12322 Human car
35	3710.5	99.7	703	8	ADU04913	Adu04913 Carcinoem
36	3701.5	99.5	701	4	AAB97817	Aab97817 Modified
37	3701.5	99.5	701	4	AAE05117	Aae05117 Modified
38	3701.5	99.5	701	5	AAB47918	Aab47918 CEA agoni
39	3700	99.4	698	2	AAR65168	Aar65168 Carcinoem
40	3700	99.4	698	2	AAW22844	Aaw22844 Human car
41	3700	99.4	698	6	ABU04822	Abu04822 Human exp
42	3700	99.4	698	6	ABU04806	Abu04806 Human exp
43	3700	99.4	698	6	ABU04798	Abu04798 Human exp
44	3700	99.4	698	6	ABU04827	Abu04827 Human exp
45	3694	99.3	702	1	AAP94014	Aap94014 Carcinoem

ALIGNMENTS

RESULT 1
ABB75931
ID ABB75931 standard; protein; 702 AA.
XX
AC ABB75931;
XX
DT 01-JUL-2002 (first entry)
XX
DE Carcinoembryonic antigen.
XX
KW Carcinoembryonic antigen; CEA; epitope; human leucocyte antigen; HLA;
KW major histocompatibility complex; MHC; CD4; T lymphocyte; cancer; tumour;
KW cytostatic; antitumour; therapy; diagnosis; human; human.
XX
OS Homo sapiens.
XX
PN WO200222803-A2.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US028467.
XX
PR 12-SEP-2000; 2000US-0232185P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz R, Tomlinson A;
XX
DR WPI; 2002-362345/39.
DR N-PSDB; ABL54023.
XX
PT Identifying human leukocyte antigen (HLA) class II-restricted epitopes,
PT comprises isolating a major histocompatibility complex (MHC) molecule
PT bound to a peptide and eluting the peptide.
XX
PS Example 1; Fig 1B; 98pp; English.
XX
CC The present sequence is the protein sequence for human carcinoembryonic
CC antigen (CEA). Epstein-Barr virus-transformed B cell lines expressing CEA
CC encoding cDNA were used to identify human leucocyte antigen (HLA) Class
CC II binding CEA peptide epitopes. The invention provides methods for
CC identifying peptide epitopes that activate CD4+ T lymphocyte responses
CC involved in the initiation, promotion, or exacerbation of certain
CC diseases. It is based on the discovery that it is possible to identify
CC human leucocyte antigen class II restricted epitopes naturally produced
CC by antigen-presenting cells transfected with DNA encoding a protein from
CC which the epitopes are derived. The method has 2 phases: immunological

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CC   mass fingerprinting, and epitope verification. By applying the methods to
CC   the tumour antigen CEA, CEA-derived peptides (see ABB75917-26) were
CC   identified as epitopes that could be involved in the pathogenesis of
CC   cancer in human patients expressing the DR4 or DR1 class II major
CC   histocompatibility complex (MHC) allele. The epitopes, and altered
CC   peptide ligands (APL), are used in claimed methods of activating T cell
CC   reactivity, altering T cell response, diagnosis, and identifying a
CC   reagent for diagnosing cancer. Also claimed are methods of cancer
CC   therapy, and of identifying a class II MHC-binding fragment of a tumour
CC   antigen. APLs are also useful as vaccines
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 5;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 2
ABU56667
ID   ABU56667 standard; protein; 702 AA.
XX
AC   ABU56667;
XX
DT   02-APR-2003  (first entry)
XX
DE   Lung cancer-associated polypeptide #260.
XX
KW   Lung cancer-associated polypeptide; cytostatic; emphysema;
KW   antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW   small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW   chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW   interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS   Unidentified.
XX
PN   WO200286443-A2.
XX
PD   31-OCT-2002.
XX
PF   18-APR-2002; 2002WO-US012476.
XX
PR   18-APR-2001; 2001US-0284770P.
PR   10-MAY-2001; 2001US-0290492P.
PR   09-NOV-2001; 2001US-0339245P.
PR   13-NOV-2001; 2001US-0350666P.
PR   29-NOV-2001; 2001US-0334370P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Aziz N,  Murray R;
XX
DR   WPI; 2003-093161/08.
DR   N-PSDB; ABX76396.
XX
PT   Detecting a lung cancer-associated transcript in a cell from a patient
PT   for treating lung cancer, by contacting a biological sample from the
PT   patient with a polynucleotide that exhibits increased or decreased
PT   expression in lung cancer.
XX
PS   Claim 27; Page 390; 453pp; English.
XX
CC   The invention relates to a method for detecting a lung cancer-associated
CC   transcript in a cell from a patient, comprising contacting a biological
CC   sample from the patient with a polynucleotide that selectively hybridises
CC   to a sequence that is at least 80 % identical to a gene that exhibits
CC   increased or decreased expression in lung cancer samples. Lung cancer-
CC   associated polynucleotides and polypeptides are used for identifying a
CC   compound that modulates a lung cancer-associated polypeptide, for
CC   inhibiting proliferation of a lung cancer-associated cell to treat lung
CC   cancer in a patient and for treating a mammal having lung cancer by
CC   administering a modulatory compound identified. The methods are useful
CC   for treating lung cancer, such as small cell lung cancer, non-small cell
CC   lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC   emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC   hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC   bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC   for diagnostic purposes and as targets for screening for therapeutic
CC   compounds that modulate lung cancer, such as antibodies. Sequences
CC   ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC   invention
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
```

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Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
                 |||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
```

RESULT 3
ABU56426
ID ABU56426 standard; protein; 702 AA.
XX
AC ABU56426;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #19.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR N-PSDB; ABX76144.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 204; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
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Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
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Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 4
ADA84059
ID   ADA84059 standard; protein; 702 AA.
XX
AC   ADA84059;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human CEACAM5 protein.
XX
KW   human; marker; expressed sequence tag; EST; arabidopsis; tumour;
KW   stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
KW   vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2002103028-A2.
XX
PD   27-DEC-2002.
XX
PF   30-MAY-2002; 2002WO-IB004189.
XX
PR   30-MAY-2001; 2001US-0293999P.
PR   22-OCT-2001; 2001US-0330457P.
PR   19-FEB-2002; 2002US-0357144P.
XX
PA   (BIOM-) BIOMEDICAL CENT.
XX
PI   Baranova AV,  Yankovsky NK,  Kozlov AP,  Lobashev AV,  Krukovskaya LL;
XX
DR   WPI; 2003-175241/17.
DR   N-PSDB; ADA84058.
XX
PT   Determining if a nucleic acid is a marker for a phenotype/cell type of
PT   interest, by global comparison of expressed sequence tags known to be
PT   expressed in the phenotype/cell type with all ESTs expressed in normal
PT   tissue.
XX
PS   Claim 29; Page 437-440; 516pp; English.
XX
CC   The invention relates to a novel method for determining if a nucleic acid
CC   is a marker for a predetermined phenotype/cell type of interest from a
CC   biological species. The method comprises performing a global comparison
CC   of a group of expressed sequence tags (ESTs) known to be expressed in the
CC   phenotype/cell type of interest with all ESTs expressed in normal tissue
CC   in order to identify ESTs that are preferentially expressed in the
CC   phenotype/cell of interest. A method of the invention is useful for
CC   determining whether a nucleic acid is a marker for a predetermined
CC   phenotype or cell type of interest from a biological species, preferably
CC   Arabidopsis or human. The cell type of interest is an abnormal cell such
CC   as a tumour cell, and the predetermined phenotype is a stress-induced
CC   phenotype such as hyperosmotic stress or high salt conditions. A method
CC   of the invention is also useful for determining the progression of colon
CC   cancer in a human, for detecting a tumour cell, and for regulating or
CC   preventing the growth of a tumour cell. An antibody of the invention is
CC   useful for detecting the absence or presence of peptides encoded by
CC   tumour-associated markers. A polypeptide of the invention is useful as an
CC   immunogen for vaccinating an animal. The present sequence represents a
CC   tumour-associated antigen of the invention.
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 5
ABP74707
ID   ABP74707 standard; protein; 702 AA.
XX
AC   ABP74707;
XX
DT   03-FEB-2003  (first entry)
XX
DE   Human CEA protein SEQ ID NO:592.
XX
KW   Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
KW   T cell.
XX
OS   Homo sapiens.
XX
PN   WO200281646-A2.
XX
```

PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US011101.
XX
PR 06-APR-2001; 2001US-0282211P.
PR 07-NOV-2001; 2001US-0337017P.
PR 07-MAR-2002; 2002US-0363210P.
XX
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JJL, Diamond DC, Liu L, Xie Z;
XX
DR WPI; 2003-067518/06.
DR N-PSDB; ABQ83855.
XX
PT Novel epitopes useful as vaccines, comprises peptides or nucleic acid
PT encoding the peptides, that are useful epitopes of target-associated
PT antigens.
XX
PS Claim 1; Page 171; 352pp; English.
XX
CC The present invention describes an isolated epitope (I) and an epitope
CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74713 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
```

RESULT 6
ABU04837
ID ABU04837 standard; protein; 702 AA.
XX
AC ABU04837;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1503.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1503; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing

```
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 7
ABU04800
ID   ABU04800 standard; protein; 702 AA.
XX
AC   ABU04800;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1466.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1466; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
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Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
```

RESULT 8
ABU04834
ID ABU04834 standard; protein; 702 AA.
XX
AC ABU04834;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1500.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1500; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 702 AA;

```
  Query Match             100.0%;  Score 3721;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
```

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Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 9
ABU04796
ID   ABU04796 standard; protein; 702 AA.
XX
AC   ABU04796;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1462.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1462; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 6;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 10
ABR82476
ID   ABR82476 standard; protein; 702 AA.
XX
AC   ABR82476;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human carcinoembryonic antigen (CEA) polypeptide.
XX
KW   CEA; immune response; carcinoembryonic antigen; antigen presenting cell;
KW   APC; cytostatic; vaccine; human; antigen.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .34
FT                   /note= "signal peptide"
FT   Protein         35. .702
FT                   /note= "mature protein"
XX
PN   WO2003059379-A2.
XX
PD   24-JUL-2003.
```

XX
PF 17-JAN-2003; 2003WO-DK000031.
XX
PR 17-JAN-2002; 2002DK-00000082.
PR 17-JAN-2002; 2002US-0350047P.
XX
PA (PHAR-) PHARMEXA AS.
XX
PI Klysner S, Voldborg B;
XX
DR WPI; 2003-587260/55.
DR N-PSDB; ACF35963.
XX
PT Inducing an immune response in humans against autologous carcinoembryonic
PT antigen (CEA) comprises administering a modified CEA polypeptide, a
PT nucleic acid encoding the polypeptide, or a microorganism expressing the
PT polypeptide.
XX
PS Claim 19; Page 100-104; 140pp; English.
XX
CC The invention relates to inducing an immune response against autologous
CC carcinoembryonic antigen (CEA) in an animal, e.g. human. The method
CC involves effecting uptake and processing by antigen presenting cells
CC (APCs) in the animal of at least 1 modified CEA polypeptide or of a
CC nucleic acid encoding the modified CEA polypeptide or of a microorganism
CC or virus expressing the modified CEA polypeptide to induce a CTL response
CC and an antibody response that targets the autologous CEA. The method is
CC useful in immunizing actively against diseases characterized by cells
CC that express CEA. The present sequence represents a human CEA polypeptide
XX
SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
Db 1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy 61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
Db 61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy 121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
Db 121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy 181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
Db 181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy 301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
Db 301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy 361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
Db 361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy 421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
Db 421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy 481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
Db 481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
Db 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy 601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
Db 601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy 661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
Db 661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702

RESULT 11
ADC09591
ID ADC09591 standard; protein; 702 AA.
XX
AC ADC09591;
XX
DT 18-DEC-2003 (first entry)
XX
DE CEA protein #SEQ ID 592.
XX
KW Epitope; immunological; vaccine;
KW major histocompatibility complex class I; MHC class I; cancer;
KW immunisation.
XX
OS Unidentified.
XX
PN WO2003008537-A2.
XX
PD 30-JAN-2003.
XX
PF 29-MAR-2002; 2002WO-US010189.
XX
PR 06-APR-2001; 2001US-0282211P.
PR 07-NOV-2001; 2001US-0337017P.
PR 07-MAR-2002; 2002US-0363210P.
XX
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JJL, Diamond DC, Liu L, Xie Z;
XX
DR WPI; 2003-248010/24.
XX
PT Epitope having high affinity for major histocompatibility complex class I
PT useful for treating an animal, evaluating immunogenicity of a vaccine or
PT therapeutic composition and for diagnosing a disease.
XX
PS Claim 1; SEQ ID NO 592; 239pp; English.
XX
CC The invention relates to an isolated epitope polypeptide that has high
CC affinity for major histocompatibility complex (MHC) class I, and an
CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine
CC or immunotherapeutic composition containing an epitope of the invention.
CC Compositions of the invention may be used in the treatment of cancer. The
CC method can be combined with a radiation therapy, chemotherapy,
CC biochemotherapy or surgery. The composition is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
CC -peptide complexes of the invention are useful for determining specific T
CC cell frequency. This method is useful for evaluating immunological
CC response, by performing the method prior to and subsequent to an
CC immunisation step. Compositions of the invention are useful for
CC diagnosing a disease. The current sequence represents an epitope of the
CC invention with high affinity for MHC class I.
XX
SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

```
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
```

```
RESULT 12
ADD25526
ID   ADD25526 standard; protein; 702 AA.
XX
AC   ADD25526;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated protein #40.
XX
KW   Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 87; 157pp; English.
XX
CC   The invention relates to a binding domain-immunoglobulin fusion protein
CC   comprising a binding domain polypeptide that is fused to an
CC   immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC   CH2 constant region polypeptide that is fused to the hinge region
CC   polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC   polypeptide that is fused to the CH2 constant region polypeptide. The
CC   hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC   hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC   region polypeptide, derived from (a) having 3 or more cysteine residues;
CC   where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC   contains 2 cysteine residues, where the first cysteine is not mutated; a
CC   mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC   (a) having 3 or more cysteine residues, where the mutated human IgG1
CC   immunoglobulin hinge region polypeptide contains no more than one
CC   cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC   polypeptide, derived from (a) having 3 or more cysteine residues; where
CC   the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC   no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC   capable of at least one immunological activity comprising antibody
CC   dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC   binding domain polypeptide is capable of specifically binding to an
CC   antigen. Also included are an isolated polynucleotide encoding the
CC   binding domain-immunoglobulin fusion protein, a recombinant expression
CC   construct comprising the polynucleotide (operably linked to a promoter),
CC   a host cell transformed or transfected with a recombinant expression
CC   construct, producing the binding domain-immunoglobulin fusion protein, a
CC   pharmaceutical composition comprising the binding domain-immunoglobulin
CC   fusion protein or polynucleotide and a carrier, and treating a subject
CC   having or suspected of having a malignant condition or a B-cell disorder.
CC   The binding domain-immunoglobulin fusion protein is useful for treating a
CC   subject having or suspected of having a malignant condition or a B-cell
CC   disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC   myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC   sclerosis or autoimmune disease. The present sequence is a binding domain
CC   -immunoglobulin fusion protein-associated protein sequence. Note: The
CC   sequence data for this patent formed part of the printed specification
CC   and is also available in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC   identified the sequences in the printed specification by their SEQ ID
CC   number therefore none of the sequences can be explicitly identified.
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 7;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
                |||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 13
ADD46175
ID   ADD46175 standard; protein; 702 AA.
XX
AC   ADD46175;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06731, SEQ ID NO 11850.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06731.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 7;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
                |||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 14
ADD84721
ID   ADD84721 standard; protein; 702 AA.
XX
AC   ADD84721;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human carcinoembryonic antigen (CEA) primary amino acid sequence.
XX
KW   identification;
KW   class I major histocompatibility complex-binding fragment;
KW   class I MHC molecule; class I MHC-binding fragment; cytostatic; cancer;
KW   human; carcinoembryonic antigen; CEA; epitope.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003082317-A1.
XX
PD   09-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008427.
XX
PR   22-MAR-2002; 2002US-0366822P.
XX
PA   (ZYCO-) ZYCOS INC.
PA   (AVET ) AVENTIS PASTEUR INC.
XX
PI   Chicz RM,  Tomlinson AJ;
XX
DR   WPI; 2003-902907/82.
XX
PT   Identifying a class I major histocompatibility complex (MHC)-binding
PT   fragment of a polypeptide comprises isolating an MHC molecule, eluting
PT   the peptide from the molecule, and identifying the peptide as a
PT   polypeptide fragment.
XX
PS   Disclosure; Fig 8; 98pp; English.
XX
CC   The present invention describes a method for identifying a class I major
CC   histocompatibility complex (MHC)-binding fragment of a polypeptide by
CC   isolating from the tissue/cell line a class I MHC molecule bound to a
CC   peptide, where the peptide is a class I MHC-binding fragment of the
CC   polypeptide, eluting the peptide from the class I MHC molecule, and
CC   identifying the peptide as a fragment of the polypeptide. A class I MHC-
CC   binding fragment has cytostatic activity. Compositions and methods from
CC   the present invention can be used in diagnosing, preventing or treating
CC   cancer. The method may also be used in identifying peptides involved in
CC   the pathogenesis of or protection from diseases associated with
CC   expression of class I MHC molecules. The present sequence represents the
CC   human carcinoembryonic antigen (CEA) primary amino acid sequence, which
CC   is used in the exemplification of the present invention.
XX
SQ   Sequence 702 AA;

  Query Match             100.0%;  Score 3721;  DB 7;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-199;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 15
ADN39014
ID   ADN39014 standard; protein; 702 AA.
XX
AC   ADN39014;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:332.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
```

XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR N-PSDB; ADN39013.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO 332; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
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Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
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Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
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Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
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Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
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Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
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Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
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Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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Search completed: April 10, 2006, 18:01:25
Job time : 275.797 secs

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:51 ; Search time 179.941 Seconds
(without alignments)
1630.072 Million cell updates/sec

Title: US-10-734-564-72
Perfect score: 3721
Sequence: 1 MESPSAPPHRWCIPWQRLLL.....LSAGATVGIMIGVLVGVALI 702

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3721	100.0	702	4	US-10-157-031-341	Sequence 341, App
2	3721	100.0	702	4	US-10-207-655-87	Sequence 87, Appl
3	3721	100.0	702	4	US-10-117-937-592	Sequence 592, App
4	3721	100.0	702	4	US-10-295-027-332	Sequence 332, App
5	3721	100.0	702	4	US-10-245-871-282	Sequence 282, App
6	3721	100.0	702	4	US-10-253-286-282	Sequence 282, App
7	3721	100.0	702	4	US-10-380-136-16	Sequence 16, Appl
8	3721	100.0	702	4	US-10-149-137A-458	Sequence 458, App
9	3721	100.0	702	4	US-10-712-124-74	Sequence 74, Appl
10	3721	100.0	702	4	US-10-734-564-72	Sequence 72, Appl
11	3721	100.0	702	4	US-10-657-022-88	Sequence 88, Appl
12	3721	100.0	702	5	US-10-473-127-1462	Sequence 1462, Ap
13	3721	100.0	702	5	US-10-473-127-1466	Sequence 1466, Ap
14	3721	100.0	702	5	US-10-473-127-1500	Sequence 1500, Ap
15	3721	100.0	702	5	US-10-473-127-1503	Sequence 1503, Ap
16	3721	100.0	702	5	US-10-696-639-65	Sequence 65, Appl
17	3721	100.0	702	5	US-10-696-639-69	Sequence 69, Appl
18	3721	100.0	702	5	US-10-482-029-241	Sequence 241, App
19	3721	100.0	702	5	US-10-893-018-2	Sequence 2, Appli
20	3721	100.0	702	5	US-10-794-514A-301	Sequence 301, App
21	3721	100.0	702	5	US-10-756-149-4748	Sequence 4748, Ap
22	3721	100.0	702	6	US-11-067-064-592	Sequence 592, App
23	3721	100.0	702	6	US-11-067-159-592	Sequence 592, App
24	3721	100.0	734	3	US-09-756-551A-17	Sequence 17, Appl
25	3721	100.0	734	5	US-10-473-127-1489	Sequence 1489, Ap
26	3718	99.9	796	5	US-10-473-127-1478	Sequence 1478, Ap
27	3701.5	99.5	701	4	US-10-168-417A-4	Sequence 4, Appli
28	3700	99.4	698	5	US-10-473-127-1464	Sequence 1464, Ap
29	3700	99.4	698	5	US-10-473-127-1472	Sequence 1472, Ap
30	3700	99.4	698	5	US-10-473-127-1488	Sequence 1488, Ap
31	3700	99.4	698	5	US-10-473-127-1493	Sequence 1493, Ap
32	3694	99.3	702	5	US-10-473-127-1483	Sequence 1483, Ap
33	3687	99.1	702	5	US-10-473-127-1485	Sequence 1485, Ap
34	3687	99.1	702	5	US-10-473-127-1491	Sequence 1491, Ap
35	3685.5	99.0	697	5	US-10-473-127-1475	Sequence 1475, Ap
36	3683	99.0	702	5	US-10-473-127-1465	Sequence 1465, Ap
37	3668	98.6	702	5	US-10-473-127-1496	Sequence 1496, Ap
38	3643	97.9	698	5	US-10-473-127-1482	Sequence 1482, Ap
39	3625	97.4	681	5	US-10-893-018-4	Sequence 4, Appli
40	3603	96.8	717	5	US-10-893-018-6	Sequence 6, Appli
41	3565	95.8	713	5	US-10-893-018-10	Sequence 10, Appl
42	3535.5	95.0	708	5	US-10-893-018-8	Sequence 8, Appli
43	3453	92.8	737	3	US-09-925-301-1133	Sequence 1133, Ap
44	3453	92.8	737	5	US-10-473-127-1476	Sequence 1476, Ap
45	3417	91.8	645	5	US-10-510-523-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-157-031-341
; Sequence 341, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequenc
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 341
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-341

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
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Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
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Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
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Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
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Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
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Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
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Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
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Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 2
US-10-207-655-87
; Sequence 87, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-207-655-87

  Query Match             100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
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Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
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Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
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Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
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Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
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Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
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RESULT 3
US-10-117-937-592
; Sequence 592, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 592
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-117-937-592

  Query Match             100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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RESULT 4
US-10-295-027-332
; Sequence 332, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-332

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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RESULT 5
US-10-245-871-282
; Sequence 282, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000

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;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 905
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-245-871-282

  Query Match            100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 6
US-10-253-286-282
; Sequence 282, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2015
;  CURRENT APPLICATION NUMBER: US/10/253,286
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 905
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-253-286-282

  Query Match            100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 7
US-10-380-136-16
; Sequence 16, Application US/10380136
; Publication No. US20040071726A1
; GENERAL INFORMATION:
;  APPLICANT: Chicz, Roman M.
```

```
;  APPLICANT:  Tomlinson, Andy
;  TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY ANTIGEN
;  TITLE OF INVENTION:  SPECIFIC CD4+ T LYMPHOCYTES
;  FILE REFERENCE: 08191-019US1
;  CURRENT APPLICATION NUMBER: US/10/380,136
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: PCT/US01/28467
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US 60/232,185
;  PRIOR FILING DATE: 2000-09-12
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-380-136-16

  Query Match           100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 8
US-10-149-137A-458
;  Sequence 458, Application US/10149137A
;  Publication No. US20040146519A1
;  GENERAL INFORMATION:
;   APPLICANT: Fikes, John
;   APPLICANT:  Sette, Alessandro
;   APPLICANT:  Sidney, John
;   APPLICANT:  Southwood, Scott
;   APPLICANT:  Chesnut, Robert
;   APPLICANT:  Celis, Esteban
;   APPLICANT:  Keogh, Elissa
;   TITLE OF INVENTION: Inducing Cellular Immune Responses to Carcinoembryonic
;   TITLE OF INVENTION:  Antigen Using Peptide and Nucleic Acid Compositions
;   FILE REFERENCE: 2060.0080006
;   CURRENT APPLICATION NUMBER: US/10/149,137A
;   CURRENT FILING DATE:  2002-06-10
;   PRIOR APPLICATION NUMBER: PCT/US00/33574
;   PRIOR FILING DATE: 2000-12-11
;   PRIOR APPLICATION NUMBER: US 09/458,302
;   PRIOR FILING DATE: 1999-12-10
;   NUMBER OF SEQ ID NOS: 562
;   SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 458
;    LENGTH: 702
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-149-137A-458

  Query Match           100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 9
US-10-712-124-74
; Sequence 74, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
;  APPLICANT: SMITH, VICTORIA
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
;  FILE REFERENCE: P2000R1
;  CURRENT APPLICATION NUMBER: US/10/712,124
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: US 60/425,813
;  PRIOR FILING DATE: 2002-11-13
;  NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 74
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-712-124-74

  Query Match             100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 10
US-10-734-564-72
; Sequence 72, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
;  APPLICANT: Christopher C Burgess et al
;  TITLE OF INVENTION: Detection Methods Using TIMP1
;  FILE REFERENCE: 1657/2012
;  CURRENT APPLICATION NUMBER: US/10/734,564
;  CURRENT FILING DATE:  2003-12-12
;  NUMBER OF SEQ ID NOS: 138
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-734-564-72

  Query Match             100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702

RESULT 11
US-10-657-022-88
; Sequence 88, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-657-022-88

  Query Match           100.0%;  Score 3721;  DB 4;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 12
US-10-473-127-1462
; Sequence 1462, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
;  APPLICANT: Zycos Inc.
;  TITLE OF INVENTION: TRANSLATIONAL PROFILING
;  FILE REFERENCE: 08191-026WO1
;  CURRENT APPLICATION NUMBER: US/10/473,127
;  CURRENT FILING DATE:  2003-09-26
;  PRIOR APPLICATION NUMBER: 60/279,495
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: 60/292,544
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: 60/310,801
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/326,370
;  PRIOR FILING DATE: 2001-10-01
;  PRIOR APPLICATION NUMBER: 60/336,780
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 60/358,985
;  PRIOR FILING DATE: 2002-02-20
;  NUMBER OF SEQ ID NOS: 2041
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1462
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-473-127-1462

  Query Match           100.0%;  Score 3721;  DB 5;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
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Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 13
US-10-473-127-1466
; Sequence 1466, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
;  APPLICANT: Zycos Inc.
;  TITLE OF INVENTION: TRANSLATIONAL PROFILING
;  FILE REFERENCE: 08191-026WO1
;  CURRENT APPLICATION NUMBER: US/10/473,127
;  CURRENT FILING DATE:  2003-09-26
;  PRIOR APPLICATION NUMBER: 60/279,495
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: 60/292,544
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: 60/310,801
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/326,370
;  PRIOR FILING DATE: 2001-10-01
;  PRIOR APPLICATION NUMBER: 60/336,780
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 60/358,985
;  PRIOR FILING DATE: 2002-02-20
;  NUMBER OF SEQ ID NOS: 2041
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1466
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-473-127-1466

  Query Match            100.0%;  Score 3721;  DB 5;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 14
US-10-473-127-1500
; Sequence 1500, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
;  APPLICANT: Zycos Inc.
;  TITLE OF INVENTION: TRANSLATIONAL PROFILING
;  FILE REFERENCE: 08191-026WO1
;  CURRENT APPLICATION NUMBER: US/10/473,127
;  CURRENT FILING DATE:  2003-09-26
;  PRIOR APPLICATION NUMBER: 60/279,495
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: 60/292,544
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: 60/310,801
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/326,370
;  PRIOR FILING DATE: 2001-10-01
;  PRIOR APPLICATION NUMBER: 60/336,780
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 60/358,985
;  PRIOR FILING DATE: 2002-02-20
;  NUMBER OF SEQ ID NOS: 2041
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1500
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-473-127-1500

  Query Match            100.0%;  Score 3721;  DB 5;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
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Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 15
US-10-473-127-1503
; Sequence 1503, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
;  APPLICANT: Zycos Inc.
;  TITLE OF INVENTION: TRANSLATIONAL PROFILING
;  FILE REFERENCE: 08191-026WO1
;  CURRENT APPLICATION NUMBER: US/10/473,127
;  CURRENT FILING DATE:  2003-09-26
;  PRIOR APPLICATION NUMBER: 60/279,495
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: 60/292,544
;  PRIOR FILING DATE: 2001-05-21
;  PRIOR APPLICATION NUMBER: 60/310,801
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/326,370
;  PRIOR FILING DATE: 2001-10-01
;  PRIOR APPLICATION NUMBER: 60/336,780
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 60/358,985
;  PRIOR FILING DATE: 2002-02-20
;  NUMBER OF SEQ ID NOS: 2041
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1503
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-473-127-1503

  Query Match           100.0%;  Score 3721;  DB 5;  Length 702;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-207;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


Search completed: April 10, 2006, 18:12:45
Job time : 181.941 secs
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OM protein - protein search, using sw model

Run on: April 10, 2006, 18:09:01 ; Search time 25.4851 Seconds
(without alignments)
859.197 Million cell updates/sec

Title: US-10-734-564-72
Perfect score: 3721
Sequence: 1 MESPSAPPHRWCIPWQRLLL.....LSAGATVGIMIGVLVGVALI 702

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3721	100.0	702	7	US-11-033-039-282	Sequence 282, App
2	3721	100.0	702	7	US-11-097-224B-2	Sequence 2, Appli
3	3721	100.0	702	7	US-11-050-857-549	Sequence 549, App
4	3721	100.0	702	7	US-11-051-720-1451	Sequence 1451, Ap
5	3721	100.0	702	7	US-11-097-252A-2	Sequence 2, Appli
6	3683	99.0	702	6	US-10-510-101-68	Sequence 68, Appl
7	3601.5	96.8	719	7	US-11-050-857-551	Sequence 551, App
8	3601.5	96.8	719	7	US-11-051-720-1381	Sequence 1381, Ap
9	2968	79.8	569	7	US-11-050-857-552	Sequence 552, App
10	2968	79.8	569	7	US-11-051-720-1382	Sequence 1382, Ap
11	1637	44.0	346	7	US-11-050-857-554	Sequence 554, App
12	1637	44.0	346	7	US-11-051-720-1384	Sequence 1384, Ap
13	1636	44.0	346	7	US-11-050-857-553	Sequence 553, App
14	1636	44.0	346	7	US-11-051-720-1383	Sequence 1383, Ap
15	1443	38.8	344	7	US-11-080-991-4	Sequence 4, Appli
16	1443	38.8	344	7	US-11-186-284-20	Sequence 20, Appl
17	1443	38.8	344	7	US-11-077-386-16	Sequence 16, Appl
18	1443	38.8	344	7	US-11-097-224B-4	Sequence 4, Appli
19	1443	38.8	344	7	US-11-050-857-56	Sequence 56, Appl
20	1443	38.8	344	7	US-11-050-857-959	Sequence 959, App
21	1443	38.8	344	7	US-11-097-252A-4	Sequence 4, Appli
22	1439	38.7	324	7	US-11-050-857-57	Sequence 57, Appl
23	1439	38.7	390	7	US-11-050-857-59	Sequence 59, Appl
24	1432	38.5	324	7	US-11-077-386-15	Sequence 15, Appl
25	1392.5	37.4	325	6	US-10-311-822-12	Sequence 12, Appl
26	1391.5	37.4	325	6	US-10-311-822-11	Sequence 11, Appl
27	1245	33.5	315	7	US-11-050-857-550	Sequence 550, App
28	1245	33.5	315	7	US-11-051-720-1380	Sequence 1380, Ap
29	1148.5	30.9	419	6	US-10-821-234-1664	Sequence 1664, Ap
30	1148.5	30.9	419	6	US-10-948-716-7	Sequence 7, Appli
31	1141.5	30.7	428	6	US-10-948-716-3	Sequence 3, Appli
32	1130.5	30.4	426	6	US-10-948-716-9	Sequence 9, Appli
33	1127.5	30.3	426	6	US-10-948-716-1	Sequence 1, Appli
34	1124.5	30.2	426	6	US-10-821-234-1585	Sequence 1585, Ap
35	1117.5	30.0	419	6	US-10-948-716-4	Sequence 4, Appli
36	1104	29.7	424	6	US-10-948-716-6	Sequence 6, Appli
37	1069	28.7	424	6	US-10-948-716-10	Sequence 10, Appl
38	1037	27.9	256	7	US-11-050-857-58	Sequence 58, Appl
39	898	24.1	335	6	US-10-948-716-2	Sequence 2, Appli
40	890	23.9	335	6	US-10-948-716-5	Sequence 5, Appli
41	638	17.1	183	7	US-11-050-857-60	Sequence 60, Appl
42	536	14.4	213	6	US-10-948-716-11	Sequence 11, Appl
43	462.5	12.4	425	6	US-10-311-822-4	Sequence 4, Appli
44	449	12.1	405	6	US-10-311-822-9	Sequence 9, Appli
45	413.5	11.1	5636	7	US-11-065-695-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-11-033-039-282
; Sequence 282, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-282

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.6e-226;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
```

```
Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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RESULT 2
US-11-097-224B-2
; Sequence 2, Application US/11097224B
; Publication No. US20060024314A1
; GENERAL INFORMATION:
; APPLICANT: Stanners,Clifford P.
; APPLICANT: Ilantzis, Christian
; APPLICANT: Ordonez-Garcia, Cosme
; APPLICANT: Taheri, Maryam
; APPLICANT: Screaton Robert A.
; APPLICANT: Fuks, Abraham
; APPLICANT: Saragovi, H. Uri
; TITLE OF INVENTION: Antibodies and Cyclic Peptides Which Bind CEA (Carcinoembryonic
; TITLE OF INVENTION: Antigens) And Their Use As Cancer Therapeutics
; FILE REFERENCE: 15037
; CURRENT APPLICATION NUMBER: US/11/097,224B
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/415,520
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/CA03/01533
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: CA 2,224,129
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: PCT/CA99/00119
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 09/637,530
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 11/041,199
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Notepad
; SEQ ID NO 2
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-097-224B-2

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.6e-226;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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RESULT 3
US-11-050-857-549
; Sequence 549, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 549
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-857-549

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.6e-226;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
```

```
Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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RESULT 4
US-11-051-720-1451
; Sequence 1451, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1451
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1451

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.6e-226;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
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Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
```

RESULT 5
US-11-097-252A-2
; Sequence 2, Application US/11097252A
; Publication No. US20060051352A1
; GENERAL INFORMATION:
; APPLICANT: Stanners, Clifford P.
; APPLICANT: Ilantzis, Christian
; APPLICANT: Ordonez-Garcia, Cosme
; TITLE OF INVENTION: CEA Binding Agents and Compositions To Reverse CEA-Mediated
; TITLE OF INVENTION: Tumorigenic Effects on Human Cancer Cells, Restore
; TITLE OF INVENTION: Sensitivity to Drug Induced Apoptosis and Uses Thereof
; FILE REFERENCE: 69029/17
; CURRENT APPLICATION NUMBER: US/11/097,252A
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: CA2,461,375
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Notepad
; SEQ ID NO 2
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-097-252A-2

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.6e-226;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
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Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702


RESULT 6
US-10-510-101-68
; Sequence 68, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
;  APPLICANT: Epimmune Inc.
;  APPLICANT:  Ishioka, Glenn
;  APPLICANT:  Fikes, John
;  APPLICANT:  Tangri, Shabnam
;  APPLICANT:  Sette, Alessandro
;  TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
;  FILE REFERENCE: 2060.009PC05
;  CURRENT APPLICATION NUMBER: US/10/510,101
;  CURRENT FILING DATE:  2004-10-05
;  PRIOR APPLICATION NUMBER: US 60/413,471
;  PRIOR FILING DATE: 2002-09-26
;  PRIOR APPLICATION NUMBER: US 10/116,118
;  PRIOR FILING DATE: 2002-04-05
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 702
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-510-101-68

  Query Match           99.0%;  Score 3683;  DB 6;  Length 702;
  Best Local Similarity  99.1%;  Pred. No. 4e-224;
  Matches  696;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVII 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 RSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLLIAKIQPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||| ||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATAGIMIGVLVGVALI 702


RESULT 7
US-11-050-857-551
; Sequence 551, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 1847.1005
;  CURRENT APPLICATION NUMBER: US/11/050,857
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 551
;   LENGTH: 719
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-050-857-551

  Query Match           96.8%;  Score 3601.5;  DB 7;  Length 719;
  Best Local Similarity  99.1%;  Pred. No. 5.4e-219;
```

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  Matches  679;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSA 685
              |||||||||||||||     || ||
Db        661 ATGRNNSIVKSITVSGKWL-PGASA 684


RESULT 8
US-11-051-720-1381
; Sequence 1381, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 1847.1002
;  CURRENT APPLICATION NUMBER: US/11/051,720
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1381
;   LENGTH: 719
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-051-720-1381

  Query Match            96.8%;  Score 3601.5;  DB 7;  Length 719;
  Best Local Similarity  99.1%;  Pred. No. 5.4e-219;
  Matches  679;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSA 685
              |||||||||||||||     || ||
Db        661 ATGRNNSIVKSITVSGKWL-PGASA 684


RESULT 9
US-11-050-857-552
; Sequence 552, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METI
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 1847.1005
;  CURRENT APPLICATION NUMBER: US/11/050,857
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 552
;   LENGTH: 569
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-050-857-552

  Query Match            79.8%;  Score 2968;  DB 7;  Length 569;
  Best Local Similarity  98.1%;  Pred. No. 2.7e-179;
  Matches  556;  Conservative    2;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDAR 567
              |||||||||||||| |||| :  :   |
Db        541 LPVSPRLQLSNGNMTLTLLSCQKERCR 567


RESULT 10
US-11-051-720-1382
; Sequence 1382, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 1847.1002
;  CURRENT APPLICATION NUMBER: US/11/051,720
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1382
;   LENGTH: 569
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-051-720-1382

  Query Match            79.8%;  Score 2968;  DB 7;  Length 569;
  Best Local Similarity  98.1%;  Pred. No. 2.7e-179;
  Matches  556;  Conservative    2;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDAR 567
              |||||||||||||| |||| :  :   |
Db        541 LPVSPRLQLSNGNMTLTLLSCQKERCR 567


RESULT 11
US-11-050-857-554
; Sequence 554, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHOD
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 1847.1005
;  CURRENT APPLICATION NUMBER: US/11/050,857
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 554
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-050-857-554

  Query Match            44.0%;  Score 1637;  DB 7;  Length 346;
  Best Local Similarity  49.3%;  Pred. No. 6.5e-96;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels  356;  Gaps    1;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
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Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYP---------------------------------------- 142
              ||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYP---------------------------------------- 142

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Db        143 ---------------------------------------------------------- 142

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Db        143 ---------------------------------------------------------- 142

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
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Db        143 ------------------------------------------------------------ 142

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Db        143 ------------------------------------------------------------ 142

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Db        143 ------------------------------------------------------------ 142

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
                                 ||||||||||||||||||||||||||||||||||||||||||
Db        143 -----------------ELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 184

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 244

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 304

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        305 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 346


RESULT 12
US-11-051-720-1384
; Sequence 1384, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 1847.1002
;  CURRENT APPLICATION NUMBER: US/11/051,720
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1384
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-051-720-1384

  Query Match             44.0%;  Score 1637;  DB 7;  Length 346;
  Best Local Similarity   49.3%;  Pred. No. 6.5e-96;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels  356;  Gaps    1;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
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Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYP---------------------------------------- 142

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Db        143 ------------------------------------------------------------ 142

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Db        143 ------------------------------------------------------------ 142

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Db        143 ------------------------------------------------------------ 142

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Db        143 ------------------------------------------------------------ 142

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Db        143 ------------------------------------------------------------ 142

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
                                 ||||||||||||||||||||||||||||||||||||||||||
Db        143 -----------------ELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 184

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 244

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 304

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        305 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 346


RESULT 13
US-11-050-857-553
; Sequence 553, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHO
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 1847.1005
;  CURRENT APPLICATION NUMBER: US/11/050,857
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 553
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-050-857-553

  Query Match             44.0%;  Score 1636;  DB 7;  Length 346;
  Best Local Similarity   49.3%;  Pred. No. 7.5e-96;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels  356;  Gaps    1;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILN-------- 232

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Db        233 ------------------------------------------------------------ 232

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Db        233 ------------------------------------------------------------ 232

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
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Db        233 ------------------------------------------------------------ 232

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Db        233 ------------------------------------------------------------ 232

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Db        233 ------------------------------------------------------------ 232

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
                                                          ||||||||||||
Db        233 ----------------------------------------------VLYGPDTPIISP 244

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 304

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
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Db        305 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 346


RESULT 14
US-11-051-720-1383
; Sequence 1383, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 1847.1002
;  CURRENT APPLICATION NUMBER: US/11/051,720
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1383
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-051-720-1383

  Query Match             44.0%;  Score 1636;  DB 7;  Length 346;
  Best Local Similarity   49.3%;  Pred. No. 7.5e-96;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels  356;  Gaps    1;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILN-------- 232

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Db        233 ------------------------------------------------------------ 232

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Db        233 ------------------------------------------------------------ 232

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Db        233 ------------------------------------------------------------ 232

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Db        233 ------------------------------------------------------------ 232

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Db        233 ------------------------------------------------------------ 232

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
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Db        233 ----------------------------------------------VLYGPDTPIISP 244

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 304

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||
Db        305 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 346


RESULT 15
US-11-080-991-4
; Sequence 4, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
;  APPLICANT: Veiby, Petter Ole
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
;  TITLE OF INVENTION:  AND OVARIAN CANCER
;  FILE REFERENCE: MRI-039
;  CURRENT APPLICATION NUMBER: US/11/080,991
;  CURRENT FILING DATE:  2005-03-11
;  PRIOR APPLICATION NUMBER: US/10/176,847
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-080-991-4

  Query Match             38.8%;  Score 1443;  DB 7;  Length 344;
  Best Local Similarity   83.9%;  Pred. No. 1e-83;
  Matches  271;  Conservative   11;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
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Db          1 MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  ||||||||||||  |:|||||||||||||||||| ||||||||||: |||||||
Db         61 NRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              || |||||||||||||| |||||||||||||| ||||||||||||| |: ||||||
Db        121 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              | ||||||||||||||| |||| :| |||  ||:|| ||| || ||| | ||||||| |
Db        181 NGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||   :|| ||||||||||||||||||:|||||||||||||||||||||||||| ||
Db        241 TISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFQQSTQELFIPNITVNNSGSYMCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPP 323
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Db        301 AHNSATGLNRTTVTMITVSGSAP 323


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Job time : 27.4851 secs

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:01 ; Search time 51.7426 Seconds
(without alignments)
1121.675 Million cell updates/sec

Title: US-10-734-564-72
Perfect score: 3721
Sequence: 1 MESPSAPPHRWCIPWQRLLL.....LSAGATVGIMIGVLVGVALI 702

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3721	100.0	702	2	US-09-949-016-6484	Sequence 6484, Ap
2	3721	100.0	734	1	US-08-389-459A-17	Sequence 17, Appl
3	3721	100.0	734	2	US-08-987-867A-17	Sequence 17, Appl
4	3721	100.0	740	2	US-09-949-016-8168	Sequence 8168, Ap
5	3700	99.4	698	1	US-08-602-725-36	Sequence 36, Appl
6	3402	91.4	642	1	US-08-217-299-1	Sequence 1, Appli
7	1600.5	43.0	464	1	US-08-602-725-32	Sequence 32, Appl
8	1600.5	43.0	464	2	US-09-949-016-6116	Sequence 6116, Ap
9	1600.5	43.0	464	2	US-09-949-016-7525	Sequence 7525, Ap
10	1443	38.8	365	2	US-09-949-016-7591	Sequence 7591, Ap
11	1424	38.3	321	6	5169835-17	Patent No. 5169835
12	1415	38.0	344	1	US-08-602-725-34	Sequence 34, Appl
13	1272	34.2	349	2	US-09-924-103-4	Sequence 4, Appli
14	1126.5	30.3	419	6	5169835-2	Patent No. 5169835
15	1099	29.5	424	6	5169835-6	Patent No. 5169835
16	773	20.8	354	6	5169835-4	Patent No. 5169835
17	739	19.9	156	2	US-09-370-838-210	Sequence 210, App
18	739	19.9	156	2	US-09-854-133-210	Sequence 210, App
19	667	17.9	248	6	5169835-15	Patent No. 5169835
20	635	17.1	141	2	US-09-924-103-2	Sequence 2, Appli
21	560.5	15.1	230	6	5169835-13	Patent No. 5169835
22	505	13.6	92	2	US-09-370-838-211	Sequence 211, App
23	505	13.6	92	2	US-09-854-133-211	Sequence 211, App
24	413.5	11.1	4126	2	US-09-953-096-4	Sequence 4, Appli
25	413.5	11.1	5518	2	US-09-953-096-2	Sequence 2, Appli
26	411	11.0	862	2	US-09-949-002-427	Sequence 427, App
27	410	11.0	847	2	US-09-949-002-328	Sequence 328, App
28	402	10.8	144	6	5169835-8	Patent No. 5169835
29	395.5	10.6	4391	2	US-10-006-011A-2	Sequence 2, Appli
30	379	10.2	143	6	5169835-18	Patent No. 5169835
31	362	9.7	1709	2	US-09-949-016-10503	Sequence 10503, A
32	351	9.4	122	6	5169835-12	Patent No. 5169835
33	343	9.2	596	1	US-08-752-307B-13	Sequence 13, Appl
34	343	9.2	596	2	US-09-707-802-13	Sequence 13, Appl
35	343	9.2	596	2	US-09-991-326-13	Sequence 13, Appl
36	317	8.5	607	1	US-08-752-307B-12	Sequence 12, Appl
37	317	8.5	607	2	US-09-707-802-12	Sequence 12, Appl
38	317	8.5	607	2	US-09-991-326-12	Sequence 12, Appl
39	311	8.4	107	2	US-09-513-999C-7818	Sequence 7818, Ap
40	307.5	8.3	848	2	US-09-787-443-44	Sequence 44, Appl
41	303.5	8.2	819	2	US-09-949-016-11044	Sequence 11044, A
42	303	8.1	1381	2	US-09-540-245A-16	Sequence 16, Appl
43	303	8.1	1381	2	US-10-289-776-16	Sequence 16, Appl
44	302.5	8.1	828	1	US-08-261-304-2	Sequence 2, Appli
45	301	8.1	1571	2	US-08-956-991-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-6484
; Sequence 6484, Application US/09949016
; Patent No. 6812339 issued 11/2/04
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6484
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6484

Query Match 100.0%; Score 3721; DB 2; Length 702;
Best Local Similarity 100.0%; Pred. No. 2.8e-271;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
                 |||||||||||||||||||||||||||||||||||||||||
Db        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
```

RESULT 2
US-08-389-459A-17
; Sequence 17, Application US/08389459A
; Patent No. 5817512
; GENERAL INFORMATION:
; APPLICANT: Morrow, Casey D. and Porter, Donna, C.
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,459A
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/087,009
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: UAG-004CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-389-459A-17

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  Query Match           100.0%;  Score 3721;  DB 1;  Length 734;
  Best Local Similarity  100.0%;  Pred. No. 3e-271;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 92

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 152

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 212

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 272

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 332

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 392

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 452

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 512

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 572

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 632

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 692

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
                |||||||||||||||||||||||||||||||||||||||||
Db        693 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 734
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RESULT 3
US-08-987-867A-17
; Sequence 17, Application US/08987867A
; Patent No. 6063384
; GENERAL INFORMATION:
; APPLICANT: C. Morrow et al.
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/987,867A
;      FILING DATE:  09-DEC-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/087,009
;      FILING DATE:  01-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Myers, Louis
;      REGISTRATION NUMBER:  35,965
;      REFERENCE/DOCKET NUMBER:  UAP-004CPDV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 742-4214
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  734 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-987-867A-17

  Query Match             100.0%;  Score 3721;  DB 2;  Length 734;
  Best Local Similarity   100.0%;  Pred. No. 3e-271;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 92

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 152

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 212

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 272

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 332

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 392

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 452

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 512

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 572

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 632

Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 692

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        693 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 734


RESULT 4
US-09-949-016-8168
; Sequence 8168, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8168
;   LENGTH: 740
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8168

  Query Match             100.0%;  Score 3721;  DB 2;  Length 740;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-271;
  Matches  702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         39 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 98

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 158

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 218

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 278

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 338

Qy        301 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 AHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNN 398

Qy        361 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 QSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTI 458

Qy        421 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 SPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQAN 518

Qy        481 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 NSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQS 578

Qy        541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISP 638
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Qy        601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNL 698

Qy        661 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        699 ATGRNNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 740


RESULT 5
US-08-602-725-36
; Sequence 36, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36663
;      REFERENCE/DOCKET NUMBER:  1090-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4091
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  698 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-602-725-36

  Query Match             99.4%;  Score 3700;  DB 1;  Length 698;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-269;
  Matches  698;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 60

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 120

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 180

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 240

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 300

Qy        305 DTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLP 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLP 360

Qy        365 VSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISPSY 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISPSY 420

Qy        425 TYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSAS 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSAS 480

Qy        485 GHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVS 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVS 540

Qy        545 PRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPPDSS 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 PRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPPDSS 600

Qy        605 YLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNLATGR 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 YLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNLATGR 660

Qy        665 NNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 702
              |||||||||||||||||||||||||||||||||||||||
Db        661 NNSIVKSITVSASGTSPGLSAGATVGIMIGVLVGVALI 698


RESULT 6
US-08-217-299-1
; Sequence 1, Application US/08217299
; Patent No. 5672513
;  GENERAL INFORMATION:
;    APPLICANT:  Mach, J. P.
;    APPLICANT:  Pelegrin, A.
;    APPLICANT:  Terskikh, A.
;    TITLE OF INVENTION:  Carcinoembryonic Antigen Derivatives
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,299
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93810214.2
;      FILING DATE:  25-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pokras, Bruce A.
;      REGISTRATION NUMBER:  32,748
;      REFERENCE/DOCKET NUMBER:  RAN 4093/096
```

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-5801
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  642 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  C-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-217-299-1

  Query Match             91.4%;  Score 3402;  DB 1;  Length 642;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-247;
  Matches  642;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 KLTIESTPFNVAEGKEVLLLVHNLPQHLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPA 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KLTIESTPFNVAEGKEVLLLVHNLPQHLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPA 60

Qy         95 YSGREIIYPNASLLIQNIIQNDTGFYTLHVIKSDLVNEEATGQFRVYPELPKPSISSNNS 154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YSGREIIYPNASLLIQNIIQNDTGFYTLHVIKSDLVNEEATGQFRVYPELPKPSISSNNS 120

Qy        155 KPVEDKDAVAFTCEPETQDATYLWWVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYK 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KPVEDKDAVAFTCEPETQDATYLWWVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYK 180

Qy        215 CETQNPVSARRSDSVILNVLYGPDAPTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVN 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CETQNPVSARRSDSVILNVLYGPDAPTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVN 240

Qy        275 GTFQQSTQELFIPNITVNNSGSYTCQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNP 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTFQQSTQELFIPNITVNNSGSYTCQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNP 300

Qy        335 VEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECG 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECG 360

Qy        395 IQNELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGN 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IQNELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGN 420

Qy        455 IQQHTQELFISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNSKPVE 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IQQHTQELFISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNSKPVE 480

Qy        515 DKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQ 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQ 540

Qy        575 NSVSANRSDPVTLDVLYGPDTPIISPPDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQ 634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 NSVSANRSDPVTLDVLYGPDTPIISPPDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQ 600

Qy        635 QHTQVLFIAKITPNNNGTYACFVSNLATGRNNSIVKSITVSA 676
              |||||||||||||||||||||||||||||||||||||||||||
Db        601 QHTQVLFIAKITPNNNGTYACFVSNLATGRNNSIVKSITVSA 642


RESULT 7
US-08-602-725-32
; Sequence 32, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36663
;      REFERENCE/DOCKET NUMBER:  1090-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4091
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  464 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-602-725-32

  Query Match             43.0%;  Score 1600.5;  DB 1;  Length 464;
  Best Local Similarity   73.0%;  Pred. No. 4.3e-112;
  Matches  309;  Conservative   30;  Mismatches   79;  Indels    5;  Gaps    2;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| || |||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              ||||||||||||||:|| |||||||||| |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
              :| || | ||:|||:|||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
               || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
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Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISP 422
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Db        425 LSP 427


RESULT 8
US-09-949-016-6116
; Sequence 6116, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6116
;   LENGTH: 464
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6116

  Query Match             43.0%;  Score 1600.5;  DB 2;  Length 464;
  Best Local Similarity   73.0%;  Pred. No. 4.3e-112;
  Matches  309;  Conservative   30;  Mismatches   79;  Indels    5;  Gaps    2;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| || |||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              ||||||||||||||:|| |||||||||| |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
               :| || | ||:|||:|||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
              || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
              ||| | |::||  | ||::  | | | | | | : | :| : |||::||| |   | :
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISP 422
              :||
Db        425 LSP 427


RESULT 9
US-09-949-016-7525
; Sequence 7525, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7525
;   LENGTH: 464
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7525

  Query Match             43.0%;  Score 1600.5;  DB 2;  Length 464;
  Best Local Similarity   73.0%;  Pred. No. 4.3e-112;
  Matches  309;  Conservative   30;  Mismatches   79;  Indels    5;  Gaps    2;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
              ||| ||  :||| |||||||||||||||:|| || |||||||||||||||||| |||
Db          5 SAPLHRVRVPWQGLLLTASLLTFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQLFG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
              ||||||||||||||:|| |||||||||| |||| ||||||||||: ||||||||| |
Db         65 YSWYKGERVDGNRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVTQNDTGFYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
              |||||||||||||| |||||||||||||| |||||||||||||||| |||||:||||
Db        125 IKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWINNQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
              |||||||||||||||| :|||||  |:|| |||||| ||| | ||| |||| |||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
               :| || | ||:|||:|||||||||| :|||||||||||||||||||||||||| |:||
Db        245 SDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCHANNS 304

Qy        305 DTGLNRTTVTTITVYAEPP---KPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQ 361
              || ||||| || |    |   || | :: :    |:|:| |||       :  |:  ||
Db        305 VTGCNRTTVKTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFFKNQ 364

Qy        362 SLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYG--PDDPT 419
              ||| | |::||  | ||::  | | | | | | : | :| : |||::||| |   | :
Db        365 SLPSSERMKLSQGNTTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLNVNYNALPQENG 424

Qy        420 ISP 422
              :||
Db        425 LSP 427


RESULT 10
US-09-949-016-7591
; Sequence 7591, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
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;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7591
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7591

  Query Match             38.8%;  Score 1443;  DB 2;  Length 365;
  Best Local Similarity   83.9%;  Pred. No. 2.1e-100;
  Matches  271;  Conservative   11;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |  |||||  |   :||: :||||||||||||||||||||||||||||||||||||||| |||||
Db         22 MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 81

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  |||||||||||||  |:||||||||||||||||||| ||||||||||: |||||||
Db         82 NRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFY 141

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              || |||||||||||||| |||||||||||||||| |||||||||||||| |: ||||||
Db        142 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYLWWV 201

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              | |||||||||||||||| |||| :| |||  ||:|| ||| || ||| | |||||||| |
Db        202 NGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGP 261

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||   :|| ||||||||||||||||||:|||||||||||||||||||||||||| ||
Db        262 TISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFQQSTQELFIPNITVNNSGSYMCQ 321

Qy        301 AHNSDTGLNRTTVTTITVYAEPP 323
              |||| |||||||||| |||    |
Db        322 AHNSATGLNRTTVTMITVSGSAP 344


RESULT 11
5169835-17
;Patent No. 5169835
;    APPLICANT: WAI-YEE, CHAN
;    TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
;    NUMBER OF SEQUENCES: 48
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/390,409
;      FILING DATE: 07-AUG-1989
;SEQ ID NO:17:
;      LENGTH: 321
5169835-17

  Query Match             38.3%;  Score 1424;  DB 6;  Length 321;
  Best Local Similarity   84.3%;  Pred. No. 4.7e-99;
  Matches  268;  Conservative   13;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |  |||||  |    ||: :|||||||||||||||||||||||||||||||||||| |||||
Db          1 MGPPSAPPCRLHFPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  |||||||||||||  |:|||||||||||||||||| ||||||||||: |||||||
Db         61 NRIGYSWYKGERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQNDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
              || |||||||||||||| |||||||||||||||| |||||||||||||| |||||:
Db        121 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPETQDTTYLWWI 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
              |||||||||||||||||||| :||||||  |:|| |||||| ||| | ||| |||| |
Db        181 NNQSLPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPVTLNVTYGPDTP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
              ||||  :|| |||||||||||||||||:|||||||||||||||||||||||||| ||||
Db        241 TISPSDTYYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQELFIPNITVNNSGSYTCH 300

Qy        301 AHNSDTGLNRTTVTTITV 318
              |:|| || ||||| || |
Db        301 ANNSVTGCNRTTVKTIIV 318


RESULT 12
US-08-602-725-34
; Sequence 34, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36663
;      REFERENCE/DOCKET NUMBER:  1090-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4091
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  344 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-602-725-34

  Query Match             38.0%;  Score 1415;  DB 1;  Length 344;
  Best Local Similarity   82.7%;  Pred. No. 2.5e-98;
  Matches  267;  Conservative   12;  Mismatches   44;  Indels    0;  Gaps    0;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
              |  |||||  |   :||: :|||||||||||||||||||||||||||||||||||| |||||
Db          1 MGPPSAPPCRLHVPWKEVLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
              :  |||||| ||||||  |:|||||||||||||||||| |||||||||: | |||||
Db         61 NRIGYSWYKAERVDGNSLIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTQIDTGFY 120

Qy        121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWV 180
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                 || |||||||||||||||| |||||||||||||| |||||||||||||| |: ||:|||
Db        121 TLQVIKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFTCEPEVQNTTYVWWV 180

Qy        181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAP 240
                 | ||||||||||||||| |||| :| |||  ||:|| ||| || ||| | |||||||| |
Db        181 NGQSLPVSPRLQLSNGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGP 240

Qy        241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQ 300
                 ||||   :|| ||||||| ||||||||||||:|||||||||||||||||||||||| ||
Db        241 TISPSKANYRPGENLNLSSHAASNPPAQYSWFINGTFQQSTQELFIPNITVNNSGSYMCQ 300

Qy        301 AHNSDTGLNRTTVTTITVYAEPP 323
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Db        301 AHNSATGLNRTTVTMITVSGSAP 323


RESULT 13
US-09-924-103-4
; Sequence 4, Application US/09924103
; Patent No. 6759045
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: IMMUNOTHERAPY FOR CHRONIC MYELOCYTIC LEUKEMIA
;  FILE REFERENCE: 018733-1055
;  CURRENT APPLICATION NUMBER: US/09/924,103
;  CURRENT FILING DATE:  2001-08-08
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-924-103-4

  Query Match             34.2%;  Score 1272;  DB 2;  Length 349;
  Best Local Similarity   76.8%;  Pred. No. 1.4e-87;
  Matches  241;  Conservative   19;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
                |||  || |||| ||||||| |||||||||:||||: | | ||||||||||||||   |
Db          5 SAPSCRWRIPWQGLLLTASLFTFWNPPTTAQLTIEAVPSNAAEGKEVLLLVHNLPQDPRG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
               |:||||| || ||:|||||   || ||||||| || ||||||||::|: :|||| ||| |
Db         65 YNWYKGETVDANRRIIGYVISNQQITPGPAYSNRETIYPNASLLMRNVTKNDTGSYTLQV 124

Qy        125 IKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNNQS 184
                || :|::|| |||| |:|| |||||||||| ||||||||||||||: ||||||| ||
Db        125 IKLNLMSEEVTGQFSVHPETPKPSISSNNSNPVEDKDAVAFTCEPETQNTTYLWWVNGQS 184

Qy        185 LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP 244
                |||||||||||||||||| :|||||    |:|| ||| ||  || | ||||||||||||||
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDVGPYECEIQNPASANFSDPVTLNVLYGPDAPTISP 244

Qy        245 LNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNS 304
                 :| | :| |||||||||||||:|||| ||||||| ||:|||||||  ||||| |    ||
Db        245 SDTYYHAGVNLNLSCHAASNPPSQYSWSVNGTFQQYTQKLFIPNITTKNSGSYACHTTNS 304

Qy        305 DTGLNRTTVTTITV 318
                || |||||  |||
Db        305 ATGRNRTTVRMITV 318


RESULT 14
5169835-2
;Patent No. 5169835
;    APPLICANT: WAI-YEE, CHAN
;    TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
;    NUMBER OF SEQUENCES: 48
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/390,409
;      FILING DATE: 07-AUG-1989
;SEQ ID NO:2:
;      LENGTH: 419
5169835-2

  Query Match             30.3%;  Score 1126.5;  DB 6;  Length 419;
  Best Local Similarity   46.9%;  Pred. No. 1.6e-76;
  Matches  234;  Conservative   54;  Mismatches  124;  Indels   87;  Gaps    3;

Qy          1 MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQ 60
                | : ||||   | |: |||||||| ||| ||||::|||: |  |:|||:||||||||
Db          1 MGTLSAPPCTQRIKWKGLLLTASLLNFWNLPTTAQVTIEAEPTKVSEGKDVLLLVHNLPQ 60

Qy         61 HLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFY 120
               :| || ||||:  |    |  ||:  :   ||||||||  | |||||||: : | | |
Db         61 NLTGYIWYKGQMRDLYHYITSYVVDGEIIIYGPAYSGRETAYSNASLLIQNVTREDAGSY 120

Qy        121 TLHVIKSDLVNEEATGQ--FRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLW 178
                |||:|| |      ||:  | :: | |||||||:|  | |  :||: ||:||| ||:|||
Db        121 TLHIIKGDDGTRGVTGRFTFTLHLETPKPSISSSNLNPRETMEAVSLTCDPETPDASYLW 180

Qy        179 WVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPD 238
                |:| ||||::  |:||  |||| |  ||:     |:|| :||||| ||| | ||:|
Db        181 WMNGQSLPMTHSLKLSETNRTLFLLGVTKYTAGPYECEIRNPVSASRSDPVTLNLL---- 236

Qy        239 APTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYT 298
                                                          | :
Db        237 ----------------------------------------------PKL--------- 239

Qy        299 CQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWV 358
                                      |||:|| || || |::| :  ||||: :| ||:||:
Db        240 ----------------------PKPYITINNLNPRENKDVLNFTCEPKSENYTYIWWL 275

Qy        359 NNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDP 418
                | |||||||::   :|| | | |||||: |||:| |::      |||| |||||||: |
Db        276 NGQSLPVSPRVKRPIENRILILPSVTRNETGPYQCEIRDRYGGIRSDPVTLNVLYGPDLP 335

Qy        419 TISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQ 478
                | ||:|||| |  | ||| | |||||||| |:   |   |:||| :|| |:|||| |
Db        336 RIYPSFTYYRSGEVLYLSCSADSNPPAQYSWTINEKFQLPGQKLFIRHITTKHSGLYVCS 395

Qy        479 ANNSASGHSRTTVKTITVS 497
                |||:|   :   |: ||
Db        396 VRNSATGKESSKSMTVEVS 414


RESULT 15
5169835-6
;Patent No. 5169835
;    APPLICANT: WAI-YEE, CHAN
;    TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
;    NUMBER OF SEQUENCES: 48
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/390,409
;      FILING DATE: 07-AUG-1989
;SEQ ID NO:6:
;      LENGTH: 424
5169835-6

  Query Match             29.5%;  Score 1099;  DB 6;  Length 424;
  Best Local Similarity   46.9%;  Pred. No. 1.9e-74;
  Matches  232;  Conservative   48;  Mismatches  127;  Indels   88;  Gaps    4;

Qy          5 SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFG 64
                ||||    | |: |||||||| ||| ||||:: ||: |  |:|||:||||||||:| |
Db          5 SAPPCTQHITWKGLLLTASLLNFWNLPTTAQVIIEAKPPKVSEGKDVLLLVHNLPQNLTG 64

Qy         65 YSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHV 124
               | ||||:  |    |  ||:   |   |||||||| :| |||||||: | | | ||||:
Db         65 YIWYKGQMTDLYHYITSYVV-DGQIIYGPAYSGRETVYSNASLLIQNVTQEDAGSYTLHI 123

Qy        125 IKSDLVNEEATGQFRV--YPELPKPSISSNNSKPVEDKDAVAFTCEPETQDATYLWWVNN 182
                ||       || | |  | | |||||||:|  | |  :||   |:||| ||:||| :|
Db        124 IKRGDGTGGVTGYFTVTLYSETPKPSISSSNLNPREVMEAVRLICDPETPDASYLWLLNG 183
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```
Qy        183 QSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTI 242
              |:||:: |||||  |||| || ||:      |:|| :|||| ||| | ||:|
Db        184 QNLPMTHRLQLSKTNRTLYLFGVTKYIAGPYECEIRNPVSASRSDPVTLNLL-------- 235

Qy        243 SPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAH 302
                                                      | :
Db        236 ----------------------------------------------PKL---------- 238

Qy        303 NSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQS 362
                                  | |:|| || || | :| :| |||| :| ||:||:| ||
Db        239 --------------------PMPYITINNLNPREKKDVLAFTCEPKSRNYTYIWWLNGQS 278

Qy        363 LPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISP 422
              ||||||::   :|| | | |||||: |||:| |::      |:|| |||||||| | | |
Db        279 LPVSPRVKRPIENRILILPSVTRNETGPYQCEIRDRYGGIRSNPVTLNVLYGPDLPRIYP 338

Qy        423 SYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNS 482
              |:|||| | || ||| | ||||||:| | |:|  |   |:|||  ||  :|||| |   ||
Db        339 SFTYYRSGENLDLSCFADSNPPAEYFWTINGKFQLSGQKLFIPQITTNHSGLYACSVRNS 398

Qy        483 ASGHSRTTVKTITVS 497
              |:|   :    : ||
Db        399 ATGKEISKSMIVKVS 413
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Search completed: April 10, 2006, 18:08:46
Job time : 53.7426 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:01 ; Search time 15.2574 Seconds
(without alignments)
1121.675 Million cell updates/sec

Title: US-10-734-564-100
Perfect score: 1124
Sequence: 1 MAPFEPLASGILLLLWLIAP.....ACLPREPGLCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1124	100.0	207	1	US-08-588-163-5	Sequence 5, Appli
2	1124	100.0	207	1	US-09-111-070-5	Sequence 5, Appli
3	1124	100.0	207	2	US-08-849-764C-5	Sequence 5, Appli
4	1124	100.0	207	2	US-09-262-087-5	Sequence 5, Appli
5	1124	100.0	207	2	US-08-463-261B-11	Sequence 11, Appl
6	1124	100.0	207	2	US-09-540-530-1	Sequence 1, Appli
7	1124	100.0	207	2	US-08-134-231C-23	Sequence 23, Appl
8	1124	100.0	207	2	US-08-728-160-23	Sequence 23, Appl
9	1124	100.0	207	2	US-10-116-064-5	Sequence 5, Appli
10	1124	100.0	254	2	US-09-949-016-9699	Sequence 9699, Ap
11	1009	89.8	184	2	US-09-452-817-1	Sequence 1, Appli
12	995	88.5	207	2	US-08-134-231C-22	Sequence 22, Appl
13	995	88.5	207	2	US-08-728-160-22	Sequence 22, Appl
14	902.5	80.3	206	2	US-08-134-231C-24	Sequence 24, Appl
15	902.5	80.3	206	2	US-08-728-160-24	Sequence 24, Appl
16	837.5	74.5	205	2	US-08-134-231C-25	Sequence 25, Appl
17	837.5	74.5	205	2	US-08-728-160-25	Sequence 25, Appl
18	579	51.5	106	2	US-09-452-817-2	Sequence 2, Appli
19	415.5	37.0	220	1	US-08-588-163-3	Sequence 3, Appli
20	415.5	37.0	220	1	US-09-111-070-3	Sequence 3, Appli
21	415.5	37.0	220	2	US-09-540-530-2	Sequence 2, Appli
22	415.5	37.0	220	2	US-08-134-231C-27	Sequence 27, Appl
23	415.5	37.0	220	2	US-09-660-107-11	Sequence 11, Appl
24	415.5	37.0	220	2	US-08-728-160-27	Sequence 27, Appl
25	415.5	37.0	220	2	US-08-803-954B-9	Sequence 9, Appli
26	407.5	36.3	218	2	US-08-849-764C-3	Sequence 3, Appli
27	407.5	36.3	218	2	US-09-262-087-3	Sequence 3, Appli
28	407.5	36.3	218	2	US-08-463-261B-9	Sequence 9, Appli
29	407.5	36.3	218	2	US-10-116-064-3	Sequence 3, Appli
30	394.5	35.1	220	2	US-08-134-231C-26	Sequence 26, Appl
31	394.5	35.1	220	2	US-08-728-160-26	Sequence 26, Appl
32	394.5	35.1	220	2	US-08-803-954B-7	Sequence 7, Appli
33	389.5	34.7	211	1	US-08-588-163-4	Sequence 4, Appli
34	389.5	34.7	211	1	US-09-111-070-4	Sequence 4, Appli
35	389.5	34.7	211	2	US-09-540-530-3	Sequence 3, Appli
36	389.5	34.7	211	2	US-08-134-231C-13	Sequence 13, Appl
37	389.5	34.7	211	2	US-08-728-160-13	Sequence 13, Appl
38	389.5	34.7	211	2	US-09-949-016-5932	Sequence 5932, Ap
39	389.5	34.7	336	2	US-09-949-016-10868	Sequence 10868, A
40	388.5	34.6	212	2	US-08-134-231C-29	Sequence 29, Appl
41	388.5	34.6	212	2	US-08-728-160-29	Sequence 29, Appl
42	384	34.2	210	2	US-08-849-764C-4	Sequence 4, Appli
43	384	34.2	210	2	US-09-262-087-4	Sequence 4, Appli
44	384	34.2	210	2	US-08-463-261B-10	Sequence 10, Appl
45	384	34.2	210	2	US-10-116-064-4	Sequence 4, Appli

ALIGNMENTS

```
RESULT 1
US-08-588-163-5
; Sequence 5, Application US/08588163
; Patent No. 5643752
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  A NOVEL TISSUE INHIBITOR OF
;    TITLE OF INVENTION:  METALLOPROTEINASES
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/588,163
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  METALLOPROTEINASES
;      CLONE:  TIMP-1
US-08-588-163-5

  Query Match             100.0%;  Score 1124;  DB 1;  Length 207;
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  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 2
US-09-111-070-5
; Sequence 5, Application US/09111070
; Patent No. 5914392
;  GENERAL INFORMATION:
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  A NOVEL TISSUE INHIBITOR OF
;    TITLE OF INVENTION:  METALLOPROTEINASES
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/111,070
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/588,163
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J.
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  METALLOPROTEINASES
;      CLONE:  TIMP-1
US-09-111-070-5

  Query Match           100.0%;  Score 1124;  DB 1;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
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Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 3
US-08-849-764C-5
; Sequence 5, Application US/08849764C
; Patent No. 6300310
;   GENERAL INFORMATION:
;        APPLICANT: GREENE, JOHN M
;                   ROSEN, CRAIG
;        TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
;                            METALLOPROTEINASE-4
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;             STREET: 9410 KEY WEST AVENUE
;             CITY: ROCKVILLE
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/849,764C
;             FILING DATE: 19-Sep-1997
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: MICHELE M. WALES
;             REGISTRATION NUMBER: 43,975
;             REFERENCE/DOCKET NUMBER: PF148US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 207 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-849-764C-5

  Query Match           100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
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Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
                 ||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 4
US-09-262-087-5
; Sequence 5, Application US/09262087
; Patent No. 6391853
;  GENERAL INFORMATION:
;    APPLICANT:  GREENE, JOHN M
;    APPLICANT:  ROSEN, CRAIG
;    TITLE OF INVENTION:  HUMAN TISSUE INHIBITOR OF
;    TITLE OF INVENTION:  METALLOPROTEINASE-4
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVE
;      CITY:  ROCKVILLE
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/262,087
;      FILING DATE:  04-MAR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/463,261
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14498
;      FILING DATE:  13-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  A. ANDERS BROOKES
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF148P1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-262-087-5

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 5
US-08-463-261B-11
; Sequence 11, Application US/08463261B
; Patent No. 6448042
;  GENERAL INFORMATION:
;    APPLICANT:  John M. Greene and Craig A. Rosen
;    TITLE OF INVENTION:  Human Tissue Inhibitor of Metalloproteinase-4
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVENE
;      CITY:  ROCKVILLE
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,261B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14498
;      FILING DATE:  13-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENLEY K. HOOVER
;      REGISTRATION NUMBER:  40,302
;      REFERENCE/DOCKET NUMBER:  PF148P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-610-5790
;      TELEFAX:  301-610-8439
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-463-261B-11

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
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Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 6
US-09-540-530-1
; Sequence 1, Application US/09540530
; Patent No. 6534635
; GENERAL INFORMATION:
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;  APPLICANT:  Miyazaki, Kaoru
;  APPLICANT:  Higashi, Shouichi
;  TITLE OF INVENTION:  MODIFIED TIMP
;  FILE REFERENCE:  159-57
;  CURRENT APPLICATION NUMBER: US/09/540,530
;  CURRENT FILING DATE:  2000-03-31
;  PRIOR APPLICATION NUMBER:  JP 95142/1999
;  PRIOR FILING DATE:  1999-04-01
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: modified TIMP
US-09-540-530-1

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 7
US-08-134-231C-23
; Sequence 23, Application US/08134231C
; Patent No. 6562596
;  GENERAL INFORMATION:
;       APPLICANT: Silbiger, Scott M.
;                  Koski, Raymond A.
;       TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
;                           Three (TIMP-3) Composition and Methods
;       NUMBER OF SEQUENCES: 42
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;            STREET: 1300 I Street, N.W.
;            CITY: Washington
;            STATE: District of Columbia
;            COUNTRY: USA
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/134,231C
;            FILING DATE: 06-Oct-1993
;            CLASSIFICATION: <Unknown>
;  INFORMATION FOR SEQ ID NO: 23:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 207 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-134-231C-23

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 8
US-08-728-160-23
; Sequence 23, Application US/08728160
; Patent No. 6683155
;  GENERAL INFORMATION:
;    APPLICANT:  Silbiger, Scott M.
;    APPLICANT:  Koski, Raymond A.
;    TITLE OF INVENTION:  Tissue Inhibitor Metalloproteinase Type
;    TITLE OF INVENTION:  Three (TIMP-3) Composition and Methods
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc./Patent Operations/KMP
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/728,160
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/134,231
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-728-160-23

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
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Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
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Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 9
US-10-116-064-5
; Sequence 5, Application US/10116064
; Patent No. 6828424
;   GENERAL INFORMATION:
;        APPLICANT: GREENE, JOHN M
;                   ROSEN, CRAIG
;        TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
;                            METALLOPROTEINASE-4
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;             STREET: 9410 KEY WEST AVE
;             CITY: ROCKVILLE
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/116,064
;             FILING DATE: 05-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/262,087
;             FILING DATE: 04-MAR-1999
;             APPLICATION NUMBER: PCT/US94/14498
;             FILING DATE: 13-FEB-1994
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 207 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-116-064-5

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-128;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 10
US-09-949-016-9699
; Sequence 9699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9699
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9699

  Query Match             100.0%;  Score 1124;  DB 2;  Length 254;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-127;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 107

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 167

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 227

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        228 GFQSRHLACLPREPGLCTWQSLRSQIA 254


RESULT 11
US-09-452-817-1
; Sequence 1, Application US/09452817
; Patent No. 6342374
; GENERAL INFORMATION:
;  APPLICANT: Carmichael, David F
;  APPLICANT:  Anderson, David C
;  APPLICANT:  Stricklin, George P
;  APPLICANT:  Welgus, Howard G
;  TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
;  TITLE OF INVENTION:  For Using Same And Recombinant-DNA Method For
;  TITLE OF INVENTION:  Manufacture Of Same
;  FILE REFERENCE: Serial No. 6342374 09/452,817
;  CURRENT APPLICATION NUMBER: US/09/452,817
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: 08/474,553
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/050,739
;  PRIOR FILING DATE: 1993-04-21
;  PRIOR APPLICATION NUMBER: 07/853,018
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: 07/517,475
;  PRIOR FILING DATE: 1990-05-01
;  PRIOR APPLICATION NUMBER: 07/320,923
;  PRIOR FILING DATE: 1989-03-08
;  PRIOR APPLICATION NUMBER: 06/784,319
;  PRIOR FILING DATE: 1985-10-04
;  PRIOR APPLICATION NUMBER: 06/699,181
;  PRIOR FILING DATE: 1985-02-05
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;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 184
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-452-817-1

  Query Match             89.8%;  Score 1009;  DB 2;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-114;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          24 CTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 CTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRF 60

Qy          84 VYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTY 143
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Db          61 VYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTY 120

Qy         144 TVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQSLR 203
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQSLR 180

Qy         204 SQIA 207
               ||||
Db         181 SQIA 184


RESULT 12
US-08-134-231C-22
; Sequence 22, Application US/08134231C
; Patent No. 6562596
;   GENERAL INFORMATION:
;        APPLICANT: Silbiger, Scott M.
;                   Koski, Raymond A.
;        TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
;                            Three (TIMP-3) Composition and Methods
;        NUMBER OF SEQUENCES: 42
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;             STREET: 1300 I Street, N.W.
;             CITY: Washington
;             STATE: District of Columbia
;             COUNTRY: USA
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/134,231C
;             FILING DATE: 06-Oct-1993
;             CLASSIFICATION: <Unknown>
;   INFORMATION FOR SEQ ID NO: 22:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 207 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-134-231C-22

  Query Match             88.5%;  Score 995;  DB 2;  Length 207;
  Best Local Similarity   87.0%;  Pred. No. 3.7e-112;
  Matches  180;  Conservative   11;  Mismatches   16;  Indels    0;  Gaps    0;

Qy           1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
               |||| |:||||||||||| |||||||||||||||||||:||||||||| |||:| ||||
Db           1 MAPFAPMASGILLLLWLTAPSRACTCVPPHPQTAFCNSDVVIRAKFVGTAEVNETALYQR 60

Qy          61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
               ||||||||:||| || || ||||:|||||||||||||| ||||||||||:| :| ||||
Db          61 YEIKMTKMFKGFSALRDAPDIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQLSNGHLHIT 120

Qy         121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
               ||||||||||:| |||||||||| |||||||||| |||||||| |||||||||| ||:|
Db         121 TCSFVAPWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDK 180

Qy         181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
               |||||||||||||||||||||:|:|
Db         181 GFQSRHLACLPREPGLCTWQSLRAQMA 207


RESULT 13
US-08-728-160-22
; Sequence 22, Application US/08728160
; Patent No. 6683155
;  GENERAL INFORMATION:
;    APPLICANT:  Silbiger, Scott M.
;    APPLICANT:  Koski, Raymond A.
;    TITLE OF INVENTION:  Tissue Inhibitor Metalloproteinase Type
;    TITLE OF INVENTION:  Three (TIMP-3) Composition and Methods
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc./Patent Operations/KMP
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/728,160
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/134,231
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-728-160-22

  Query Match             88.5%;  Score 995;  DB 2;  Length 207;
  Best Local Similarity   87.0%;  Pred. No. 3.7e-112;
  Matches  180;  Conservative   11;  Mismatches   16;  Indels    0;  Gaps    0;

Qy           1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
               |||| |:||||||||||| |||||||||||||||||||:||||||||| |||:| ||||
Db           1 MAPFAPMASGILLLLWLTAPSRACTCVPPHPQTAFCNSDVVIRAKFVGTAEVNETALYQR 60

Qy          61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
               ||||||||:||| || || ||||:|||||||||||||| ||||||||||:| :| ||||
Db          61 YEIKMTKMFKGFSALRDAPDIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQLSNGHLHIT 120

Qy         121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
               ||||||||||:| |||||||||| |||||||||| |||||||| |||||||||| ||:|
Db         121 TCSFVAPWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDK 180

Qy         181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db         181 GFQSRHLACLPREPGLCTWQSLRAQMA 207


RESULT 14
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US-08-134-231C-24
; Sequence 24, Application US/08134231C
; Patent No. 6562596
;   GENERAL INFORMATION:
;        APPLICANT: Silbiger, Scott M.
;                   Koski, Raymond A.
;        TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
;                            Three (TIMP-3) Composition and Methods
;        NUMBER OF SEQUENCES: 42
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;             STREET: 1300 I Street, N.W.
;             CITY: Washington
;             STATE: District of Columbia
;             COUNTRY: USA
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/134,231C
;             FILING DATE: 06-Oct-1993
;             CLASSIFICATION: <Unknown>
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 206 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-134-231C-24

  Query Match             80.3%;  Score 902.5;  DB 2;  Length 206;
  Best Local Similarity   80.8%;  Pred. No. 6e-101;
  Matches  164;  Conservative   13;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||   ||| :||||||:||||||||||||||||||||||||||||| |||| ||||||
Db          1 MAPLAALASSMLLLLWLVAPSRACTCVPPHPQTAFCNSDLVIRAKFVGAPEVNHTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |||| |||:||| ||| | |||||||||||||||| |:| ||||||||||:|::||||||
Db         61 YEIKTTKMFKGFDALGHATDIRFVYTPAMESVCGYSHKSQNRSEEFLIAGQLRNGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||| |||||| :|| ||||||  ||: |||| | |||| |:| ||||||  | ||:|
Db        121 TCSFVVPWNSLSFSQRSGFTKTYAAGCDMCTVFACASIPCHLESDTHCLWTDSSL-GSDK 179

Qy        181 GFQSRHLACLPREPGLCTWQSLR 203
              ||||||||||:||||| |:|||
Db        180 GFQSRHLACLPQEPGLCAWESLR 202


RESULT 15
US-08-728-160-24
; Sequence 24, Application US/08728160
; Patent No. 6683155
;  GENERAL INFORMATION:
;    APPLICANT:  Silbiger, Scott M.
;    APPLICANT:  Koski, Raymond A.
;    TITLE OF INVENTION:  Tissue Inhibitor Metalloproteinase Type
;    TITLE OF INVENTION:  Three (TIMP-3) Composition and Methods
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc./Patent Operations/KMP
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/728,160
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/134,231
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  206 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-728-160-24

  Query Match             80.3%;  Score 902.5;  DB 2;  Length 206;
  Best Local Similarity   80.8%;  Pred. No. 6e-101;
  Matches  164;  Conservative   13;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||   ||| :||||||:||||||||||||||||||||||||||||| |||| ||||||
Db          1 MAPLAALASSMLLLLWLVAPSRACTCVPPHPQTAFCNSDLVIRAKFVGAPEVNHTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |||| |||:||| ||| | |||||||||||||||| |:| ||||||||||:|::||||||
Db         61 YEIKTTKMFKGFDALGHATDIRFVYTPAMESVCGYSHKSQNRSEEFLIAGQLRNGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||| |||||| :|| ||||||  ||: |||| | |||| |:| ||||||  | ||:|
Db        121 TCSFVVPWNSLSFSQRSGFTKTYAAGCDMCTVFACASIPCHLESDTHCLWTDSSL-GSDK 179

Qy        181 GFQSRHLACLPREPGLCTWQSLR 203
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Db        180 GFQSRHLACLPQEPGLCAWESLR 202


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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:51 ; Search time 53.0594 Seconds
(without alignments)
1630.072 Million cell updates/sec

Title: US-10-734-564-100
Perfect score: 1124
Sequence: 1 MAPFEPLASGILLLLWLIAP.....ACLPREPGLCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1124	100.0	207	4	US-10-116-064-5	Sequence 5, Appli
2	1124	100.0	207	4	US-10-348-167-23	Sequence 23, Appl
3	1124	100.0	207	4	US-10-301-822-205	Sequence 205, App
4	1124	100.0	207	4	US-10-087-188-4	Sequence 4, Appli
5	1124	100.0	207	4	US-10-325-446-1	Sequence 1, Appli
6	1124	100.0	207	4	US-10-712-124-70	Sequence 70, Appl
7	1124	100.0	207	4	US-10-734-564-100	Sequence 100, App
8	1124	100.0	207	5	US-10-486-090-9	Sequence 9, Appli
9	1124	100.0	207	5	US-10-971-461-20	Sequence 20, Appl
10	1124	100.0	207	5	US-10-852-335A-129	Sequence 129, App
11	1124	100.0	207	5	US-10-971-195-4	Sequence 4, Appli
12	1124	100.0	207	6	US-11-037-713-52	Sequence 52, Appl
13	1120	99.6	207	3	US-09-731-872-291	Sequence 291, App
14	1120	99.6	207	3	US-09-876-997-291	Sequence 291, App
15	1120	99.6	207	5	US-10-643-836-291	Sequence 291, App
16	1034	92.0	204	4	US-10-264-049-3338	Sequence 3338, Ap
17	1010	89.9	580	4	US-10-025-514-18	Sequence 18, Appl
18	1010	89.9	580	6	US-11-077-276-18	Sequence 18, Appl
19	1009	89.8	184	4	US-10-025-514-6	Sequence 6, Appli
20	1009	89.8	184	6	US-11-077-276-6	Sequence 6, Appli
21	1009	89.8	580	4	US-10-025-514-10	Sequence 10, Appl
22	1009	89.8	580	6	US-11-077-276-10	Sequence 10, Appl
23	995	88.5	207	4	US-10-348-167-22	Sequence 22, Appl
24	902.5	80.3	206	4	US-10-348-167-24	Sequence 24, Appl
25	895	79.6	166	4	US-10-372-683-6	Sequence 6, Appli
26	837.5	74.5	205	4	US-10-348-167-25	Sequence 25, Appl
27	782.5	69.6	183	3	US-09-925-301-1594	Sequence 1594, Ap
28	728.5	64.8	212	4	US-10-264-049-3513	Sequence 3513, Ap
29	715	63.6	162	4	US-10-264-049-3566	Sequence 3566, Ap
30	691	61.5	128	4	US-10-025-514-24	Sequence 24, Appl
31	691	61.5	128	6	US-11-077-276-24	Sequence 24, Appl
32	683	60.8	522	4	US-10-025-514-20	Sequence 20, Appl
33	683	60.8	522	6	US-11-077-276-20	Sequence 20, Appl
34	682	60.7	127	4	US-10-025-514-22	Sequence 22, Appl
35	682	60.7	127	6	US-11-077-276-22	Sequence 22, Appl
36	682	60.7	522	4	US-10-025-514-14	Sequence 14, Appl
37	682	60.7	522	6	US-11-077-276-14	Sequence 14, Appl
38	587.5	52.3	136	6	US-11-097-369-2	Sequence 2, Appli
39	485	43.1	92	4	US-10-425-115-202109	Sequence 202109,
40	415.5	37.0	220	4	US-10-348-167-27	Sequence 27, Appl
41	415.5	37.0	220	4	US-10-325-446-2	Sequence 2, Appli
42	415.5	37.0	220	5	US-10-804-937A-7	Sequence 7, Appli
43	415.5	37.0	220	5	US-10-486-090-10	Sequence 10, Appl
44	415.5	37.0	220	5	US-10-971-461-21	Sequence 21, Appl
45	415.5	37.0	220	5	US-10-893-323-9	Sequence 9, Appli

ALIGNMENTS

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RESULT 1
US-10-116-064-5
; Sequence 5, Application US/10116064
; Publication No. US20020115187A1
;   GENERAL INFORMATION:
;        APPLICANT: GREENE, JOHN M
;                   ROSEN, CRAIG
;        TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
;                            METALLOPROTEINASE-4
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;             STREET: 9410 KEY WEST AVE
;             CITY: ROCKVILLE
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/116,064
;             FILING DATE: 05-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/262,087
;             FILING DATE: 04-MAR-1999
;             APPLICATION NUMBER: PCT/US94/14498
;             FILING DATE: 13-FEB-1994
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 207 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-116-064-5

  Query Match             100.0%;  Score 1124;  DB 4;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 2
US-10-348-167-23
; Sequence 23, Application US/10348167
; Publication No. US20030143693A1
;   GENERAL INFORMATION:
;        APPLICANT: Silbiger, Scott M.
;                   Koski, Raymond A.
;        TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
;                            Three (TIMP-3) Composition and Methods
;        NUMBER OF SEQUENCES: 42
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;             STREET: 1300 I Street, N.W.
;             CITY: Washington
;             STATE: District of Columbia
;             COUNTRY: USA
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/348,167
;             FILING DATE: 22-Jan-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/134,231
;             FILING DATE: October 6, 1993
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 207 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-348-167-23

  Query Match             100.0%;  Score 1124;  DB 4;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 3
US-10-301-822-205
; Sequence 205, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Berger, Allison
;  APPLICANT:  Guillemette, Tracy L.
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Schlegel, Robert
;  APPLICANT:  Monahan, John E.
;  APPLICANT:  Thibodeau, Stephen N.
;  APPLICANT:  Burgart, Lawrence J.
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;  TITLE OF INVENTION:  METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF COLON CANCER
;  FILE REFERENCE: MPM01-029P2RNM
;  CURRENT APPLICATION NUMBER: US/10/301,822
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 60/339,971
;  PRIOR FILING DATE: 2001-12-10
;  PRIOR APPLICATION NUMBER: US 60/361,978
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US 60/381,988
;  PRIOR FILING DATE: 2002-05-20
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-301-822-205

  Query Match             100.0%;  Score 1124;  DB 4;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 4
US-10-087-188-4
; Sequence 4, Application US/10087188
; Publication No. US20030175686A1
; GENERAL INFORMATION:
;  APPLICANT: Rose, Steven L.
;  APPLICANT:  Oh, Esther H.
;  APPLICANT:  Walsh, Michael
;  TITLE OF INVENTION: Methods of Diagnosing Liver Fibrosis
;  FILE REFERENCE: P-PM 4978
;  CURRENT APPLICATION NUMBER: US/10/087,188
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 10/087,188
;  PRIOR FILING DATE: 2002-02-28
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-087-188-4

Query Match 100.0%; Score 1124; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

RESULT 5
US-10-325-446-1
; Sequence 1, Application US/10325446
; Publication No. US20040121438A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Quirk
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: Wound Care Compositions
; FILE REFERENCE: 1443.048US1
; CURRENT APPLICATION NUMBER: US/10/325,446
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-446-1

Query Match 100.0%; Score 1124; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

RESULT 6
US-10-712-124-70
; Sequence 70, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425,813
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 70
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-712-124-70

Query Match 100.0%; Score 1124; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

RESULT 7
US-10-734-564-100
; Sequence 100, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using TIMP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734,564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-564-100

Query Match 100.0%; Score 1124; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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RESULT 8
US-10-486-090-9
; Sequence 9, Application US/10486090
; Publication No. US20040235724A1

```
; GENERAL INFORMATION:
;  APPLICANT: Berdel, Wolfgang E.
;  APPLICANT:  Oelmann, Elisabeth
;  TITLE OF INVENTION: Use of TIMP-1 as an Immunosuppressant
;  FILE REFERENCE: 19235.002
;  CURRENT APPLICATION NUMBER: US/10/486,090
;  CURRENT FILING DATE:  2004-02-06
;  PRIOR APPLICATION NUMBER: PCT/EP02/08733
;  PRIOR FILING DATE: 2002-08-05
;  PRIOR APPLICATION NUMBER: DE 101 38 550.1
;  PRIOR FILING DATE: 2001-08-06
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-486-090-9

  Query Match             100.0%;  Score 1124;  DB 5;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 9
US-10-971-461-20
; Sequence 20, Application US/10971461
; Publication No. US20050070477A1
; GENERAL INFORMATION:
;  APPLICANT: Cochrane, Charles G.
;  APPLICANT:  The Scripps Research Institute
;  TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
;  FILE REFERENCE: 1361.037US1
;  CURRENT APPLICATION NUMBER: US/10/971,461
;  CURRENT FILING DATE:  2004-10-22
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-971-461-20

  Query Match             100.0%;  Score 1124;  DB 5;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 10
US-10-852-335A-129
; Sequence 129, Application US/10852335A
; Publication No. US20050112129A1
; GENERAL INFORMATION:
;  APPLICANT: HEIDI S. PHILLIPS
;  TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
;  TITLE OF INVENTION:  Treatment of Tumors of Glial Origin
;  FILE REFERENCE: P5103R1-US
;  CURRENT APPLICATION NUMBER: US/10/852,335A
;  CURRENT FILING DATE:  2004-05-24
;  PRIOR APPLICATION NUMBER: US 60/548,299
;  PRIOR FILING DATE: 2004-02-27
;  PRIOR APPLICATION NUMBER: US 60/473,238
;  PRIOR FILING DATE: 2003-05-23
;  NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 129
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-852-335A-129

  Query Match             100.0%;  Score 1124;  DB 5;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 11
US-10-971-195-4
; Sequence 4, Application US/10971195
; Publication No. US20050186561A1
; GENERAL INFORMATION:
;  APPLICANT: Oh, Esther H.
;  APPLICANT:  Smith, Catherine M.
;  APPLICANT:  Prometheus Laboratories Inc.
;  TITLE OF INVENTION: Methods of Diagnosing Tissue Fibrosis
;  FILE REFERENCE: 021825-001310US
;  CURRENT APPLICATION NUMBER: US/10/971,195
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 60/514,034
;  PRIOR FILING DATE: 2003-10-24
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   OTHER INFORMATION: human tissue inhibitor of metalloproteinase-1
;   OTHER INFORMATION: (TIMP-1)
US-10-971-195-4

  Query Match             100.0%;  Score 1124;  DB 5;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 12
US-11-037-713-52
; Sequence 52, Application US/11037713
; Publication No. US20050221398A1
; GENERAL INFORMATION:
;  APPLICANT: JACQUEMIER, JOCELYNE
;  APPLICANT:  BERTUCCI, FRANCOIS
;  APPLICANT:  BIRNBAUM, DANIEL
;  APPLICANT:  DEBONO, STEPHANE
;  APPLICANT:  TAGETT, REBECCA
;  TITLE OF INVENTION: PROTEIN EXPRESSION PROFILING AND BREAST CANCER
;  TITLE OF INVENTION:  PROGNOSIS
;  FILE REFERENCE: 1016-R-04(B)
;  CURRENT APPLICATION NUMBER: US/11/037,713
;  CURRENT FILING DATE:  2005-01-18
;  PRIOR APPLICATION NUMBER: 60/537,412
;  PRIOR FILING DATE: 2004-01-16
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-037-713-52

  Query Match             100.0%;  Score 1124;  DB 6;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 13
US-09-731-872-291
; Sequence 291, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean Baptiste
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Jobert, Severin
;  TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
;  FILE REFERENCE: 78.US3.REG
;  CURRENT APPLICATION NUMBER: US/09/731,872
;  CURRENT FILING DATE:  2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/169,629
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: US 60/187,470
;  PRIOR FILING DATE: 2000-03-06
;  NUMBER OF SEQ ID NOS: 482
;  SOFTWARE: Patent.pm
; SEQ ID NO 291
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -23..-1
US-09-731-872-291

  Query Match             99.6%;  Score 1120;  DB 3;  Length 207;
  Best Local Similarity   99.5%;  Pred. No. 2.9e-111;
  Matches  206;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
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Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSFPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 14
US-09-876-997-291
; Sequence 291, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean Baptiste
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Jobert, Severin
;  TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
;  FILE REFERENCE: 78.US4.CIP
;  CURRENT APPLICATION NUMBER: US/09/876,997
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/731,872
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/187,470
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 60/169,629
;  PRIOR FILING DATE: 1999-12-08
;  NUMBER OF SEQ ID NOS: 482
;  SOFTWARE: Patent.pm
; SEQ ID NO 291
;   LENGTH: 207
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -23..-1
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US-09-876-997-291

Query Match 99.6%; Score 1120; DB 3; Length 207;
Best Local Similarity 99.5%; Pred. No. 2.9e-111;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSFPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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RESULT 15
US-10-643-836-291
; Sequence 291, Application US/10643836
; Publication No. US20050096458A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/10/643,836
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US/09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 291
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23..-1
US-10-643-836-291

Query Match 99.6%; Score 1120; DB 5; Length 207;
Best Local Similarity 99.5%; Pred. No. 2.9e-111;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSFPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Search completed: April 10, 2006, 18:12:43
Job time : 54.0594 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:09:01 ; Search time 7.51485 Seconds
(without alignments)
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Title: US-10-734-564-100
Perfect score: 1124
Sequence: 1 MAPFEPLASGILLLLWLIAP.....ACLPREPGLCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1124	100.0	207	7	US-11-186-284-205	Sequence 205, App
2	1124	100.0	254	6	US-10-821-234-861	Sequence 861, App
3	1058	94.1	197	7	US-11-094-519A-34	Sequence 34, Appl
4	1050	93.4	211	7	US-11-094-519A-32	Sequence 32, Appl
5	837	74.5	164	7	US-11-094-519A-30	Sequence 30, Appl
6	830.5	73.9	160	7	US-11-094-519A-33	Sequence 33, Appl
7	782	69.6	143	7	US-11-094-519A-52	Sequence 52, Appl
8	601	53.5	123	7	US-11-094-519A-31	Sequence 31, Appl
9	577	51.3	108	7	US-11-044-640-13	Sequence 13, Appl
10	551	49.0	147	7	US-11-094-519A-49	Sequence 49, Appl
11	526	46.8	115	7	US-11-094-519A-51	Sequence 51, Appl
12	389.5	34.7	211	6	US-10-821-234-1467	Sequence 1467, Ap
13	232	20.6	82	7	US-11-094-519A-50	Sequence 50, Appl
14	90.5	8.1	1963	6	US-10-877-346-43	Sequence 43, Appl
15	80.5	7.2	304	7	US-11-098-686-10425	Sequence 10425, A
16	75.5	6.7	283	7	US-11-087-099-12255	Sequence 12255, A
17	75	6.7	259	6	US-10-995-561-883	Sequence 883, App
18	75	6.7	764	7	US-11-075-047A-4	Sequence 4, Appli
19	75	6.7	767	7	US-11-043-693-2	Sequence 2, Appli
20	75	6.7	1306	6	US-10-995-561-905	Sequence 905, App
21	75	6.7	1356	6	US-10-995-561-904	Sequence 904, App
22	75	6.7	1356	6	US-10-995-561-906	Sequence 906, App
23	74	6.6	764	7	US-11-104-110-8	Sequence 8, Appli
24	74	6.6	764	7	US-11-104-111-28	Sequence 28, Appl
25	72	6.4	285	7	US-11-051-720-1493	Sequence 1493, Ap
26	72	6.4	665	7	US-11-051-720-1497	Sequence 1497, Ap
27	72	6.4	782	7	US-11-051-720-1496	Sequence 1496, Ap
28	71.5	6.4	326	7	US-11-037-243-105	Sequence 105, App
29	71.5	6.4	473	7	US-11-075-185-12	Sequence 12, Appl
30	71.5	6.4	552	6	US-10-131-826A-332	Sequence 332, App
31	71.5	6.4	552	6	US-10-973-115B-332	Sequence 332, App
32	70.5	6.3	415	7	US-11-182-946-6	Sequence 6, Appli
33	70.5	6.3	933	7	US-11-072-512-2928	Sequence 2928, Ap
34	70.5	6.3	1588	6	US-10-453-195-2	Sequence 2, Appli
35	70	6.2	651	7	US-11-198-819-22	Sequence 22, Appl
36	69.5	6.2	375	7	US-11-096-568A-12741	Sequence 12741, A
37	69	6.1	1198	6	US-10-877-346-35	Sequence 35, Appl
38	69	6.1	1433	7	US-11-114-962-1	Sequence 1, Appli
39	68.5	6.1	424	7	US-11-098-686-10348	Sequence 10348, A
40	68.5	6.1	1419	7	US-11-114-962-3	Sequence 3, Appli
41	67.5	6.0	229	7	US-11-087-099-2977	Sequence 2977, Ap
42	67	6.0	378	7	US-11-096-568A-9995	Sequence 9995, Ap
43	67	6.0	407	7	US-11-096-568A-9994	Sequence 9994, Ap
44	67	6.0	418	7	US-11-109-156-2	Sequence 2, Appli
45	67	6.0	449	7	US-11-096-568A-9993	Sequence 9993, Ap

ALIGNMENTS

RESULT 1
US-11-186-284-205
; Sequence 205, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-205

Query Match 100.0%; Score 1124; DB 7; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.3e-115;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db      * 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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RESULT 2
US-10-821-234-861
; Sequence 861, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 861
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-861

Query Match 100.0%; Score 1124; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 3e-115;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db         48 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 107

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 167

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 227

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        228 GFQSRHLACLPREPGLCTWQSLRSQIA 254
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RESULT 3
US-11-094-519A-34
; Sequence 34, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-094-519A-34

Query Match 94.1%; Score 1058; DB 7; Length 197;
Best Local Similarity 95.2%; Pred. No. 3.6e-108;
Matches 197; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||          ||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHR----------AGKLQDGLLHIT 110

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 170

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        171 GFQSRHLACLPREPGLCTWQSLRSQIA 197
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RESULT 4
US-11-094-519A-32
; Sequence 32, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-32

Query Match 93.4%; Score 1050; DB 7; Length 211;
Best Local Similarity 94.8%; Pred. No. 2.9e-107;
Matches 200; Conservative 1; Mismatches 6; Indels 4; Gaps 4;

```
Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLI-AGKLQDGLL-H 118
              ||||||||||||||||||||||||||||||||||||||||||||||||  |||||| : |
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLILLGKLQDGIFAH 120

Qy        119 ITTCSFV-APW-NSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQ 176
                ||||   || ||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SLTCSFCWVPWENSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQ 180

Qy        177 GSEKGFQSRHLACLPREPGLCTWQSLRSQIA 207
              ||||||||||||||||||||||||||||||
Db        181 GSEKGFQSRHLACLPREPGLCTWQSLRSQIA 211
```

RESULT 5
US-11-094-519A-30
; Sequence 30, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne

```
;  APPLICANT:  LEVINE, Zurit
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE:  2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-094-519A-30

  Query Match             74.5%;  Score 837;  DB 7;  Length 164;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-84;
  Matches  155;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPC 155
              |||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPC 155


RESULT 6
US-11-094-519A-33
; Sequence 33, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
;  APPLICANT: BERNSTEIN, Jeanne
;  APPLICANT:  LEVINE, Zurit
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE:  2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-094-519A-33

  Query Match             73.9%;  Score 830.5;  DB 7;  Length 160;
  Best Local Similarity   77.3%;  Pred. No. 2.1e-83;
  Matches  160;  Conservative    0;  Mismatches    0;  Indels   47;  Gaps    1;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLI------------ 108

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
                                                  |||||||||||||||||||||||||
Db        109 ---------------------------------LSIPCKLQSGTHCLWTDQLLQGSEK 133

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              ||||||||||||||||||||||||||
Db        134 GFQSRHLACLPREPGLCTWQSLRSQIA 160


RESULT 7
US-11-094-519A-52
; Sequence 52, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
;  APPLICANT: BERNSTEIN, Jeanne
;  APPLICANT:  LEVINE, Zurit
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE:  2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
;   LENGTH: 143
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-094-519A-52

  Query Match             69.6%;  Score 782;  DB 7;  Length 143;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-78;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         65 MTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTCSF 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTCSF 60

Qy        125 VAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQS 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQS 120

Qy        185 RHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||
Db        121 RHLACLPREPGLCTWQSLRSQIA 143


RESULT 8
US-11-094-519A-31
; Sequence 31, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
;  APPLICANT: BERNSTEIN, Jeanne
;  APPLICANT:  LEVINE, Zurit
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE:  2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-094-519A-31

  Query Match             53.5%;  Score 601;  DB 7;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-58;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ 113
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ 113


RESULT 9
US-11-044-640-13
; Sequence 13, Application US/11044640
; Publication No. US20060002969A1
; GENERAL INFORMATION:
;  APPLICANT: Kyriakides , Themis
;  APPLICANT:  Bornstein, Paul
;  TITLE OF INVENTION: METHODS FOR REDUCING THE FOREIGN BODY REACTION
;  FILE REFERENCE: UWOTL124322
;  CURRENT APPLICATION NUMBER: US/11/044,640
;  CURRENT FILING DATE:  2005-01-26
;  PRIOR APPLICATION NUMBER: US 60/539,821
;  PRIOR FILING DATE: 2004-01-27
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-11-044-640-13

  Query Match             51.3%;  Score 577;  DB 7;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-56;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLI 108
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLI 108


RESULT 10
US-11-094-519A-49
; Sequence 49, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
;  APPLICANT: BERNSTEIN, Jeanne
;  APPLICANT:  LEVINE, Zurit
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE:  2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 147
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(147)
;   OTHER INFORMATION: any Xaa is any amino acid, unknown, or other
US-11-094-519A-49

  Query Match             49.0%;  Score 551;  DB 7;  Length 147;
  Best Local Similarity   68.4%;  Pred. No. 7e-53;
  Matches  119;  Conservative    3;  Mismatches   20;  Indels   32;  Gaps    6;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||| |||||||||||||||||||||||||           |: |
Db         61 YEIKMTKMYKGFQALXDAADIRFVYTPAMESVCGYFHRSHNRSR----------GVSH-- 108

Qy        121 TCSFVAPWNSLSLA----QRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLW 170
               |   | |   :||    | ||  :          | ||    |    || |
Db        109 -CWKTAGW---TLAHHYLQFRGSLEQ----------PELSSAPGLHQDLHC-W 146


RESULT 11
US-11-094-519A-51
; Sequence 51, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
;  APPLICANT: BERNSTEIN, Jeanne
;  APPLICANT:  LEVINE, Zurit
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE:  2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-094-519A-51

  Query Match             46.8%;  Score 526;  DB 7;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-50;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHR 98
              ||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHR 98


RESULT 12
US-10-821-234-1467
; Sequence 1467, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1467
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-1467

  Query Match             34.7%;  Score 389.5;  DB 6;  Length 211;
```

```
  Best Local Similarity   39.6%;  Pred. No. 5e-35;
  Matches   78;  Conservative   38;  Mismatches   66;  Indels   15;  Gaps    7;

Qy         10 GILLLL--WLIAP--SRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQ---TTLYQRYE 62
              |:::||  | :    : |||| | ||| ||||||:||||| ||   | :    ||   |
Db          6 GLIVLLGSWSLGDWGAEACTCSPSHPQDAFCNSDIVIRAKVVGKKLVKEGPFGTLV--YT 63

Qy         63 IKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTC 122
              ||  |||:||  :     :::::| | ||:||   :      ::|: |:: || ::   |
Db         64 IKQMKMYRGFTKM---PHVQYIHTEASESLCGL--KLEVNKYQYLLTGRVYDGKMYTGLC 118

Qy        123 SFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGF 182
              :||  |: |:|:||:|    | :||  | :  |  :|| : |   |||||  |      |:
Db        119 NFVERWDQLTLSQRKGLNYRYHLGC-NCKIKSCYYLPCFVTSKNECLWTDMLSNFGYPGY 177

Qy        183 QSRHLACLPREPGLCTW 199
              ||:| ||: :: | |:|
Db        178 QSKHYACIRQKGGYCSW 194


RESULT 13
US-11-094-519A-50
; Sequence 50, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
;  APPLICANT: BERNSTEIN, Jeanne
;  APPLICANT:  LEVINE, Zurit
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE:  2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-094-519A-50

  Query Match             20.6%;  Score 232;  DB 7;  Length 82;
  Best Local Similarity   95.6%;  Pred. No. 2.6e-18;
  Matches   43;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 KMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGK 111
              :|||||||||||||||||||||||||||||||||||||||||||:
Db         13 QMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGE 57


RESULT 14
US-10-877-346-43
; Sequence 43, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
;  APPLICANT: Gerlach, Valerie L
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Stone, David
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Leach, Martin D
;  APPLICANT:  Shimkets, Richard A
;  TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-124
;  CURRENT APPLICATION NUMBER: US/10/877,346
;  CURRENT FILING DATE:  2004-06-25
;  PRIOR APPLICATION NUMBER: US/09/964,956
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,631
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/235,633
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/235,808
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,064
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,065
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,066
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,135
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: 60/237,434
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/238,321
;  PRIOR FILING DATE: 2000-10-05
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
;   LENGTH: 1963
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-877-346-43

  Query Match             8.1%;  Score 90.5;  DB 6;  Length 1963;
  Best Local Similarity   22.4%;  Pred. No. 0.39;
  Matches   46;  Conservative   19;  Mismatches   97;  Indels   43;  Gaps    7;

Qy         10 GILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTK-- 67
              | | | ||:     ||  |      ||  |  |     |: |   |||     :||
Db        448 GNLELNWLLGKDVQCTKAPVPIDDNFCGLD--INQPLGGSTPVEGLTLYTTSRDRMTSVA 505

Qy         68 --MYKGFQAL------GDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHI 119
                :| |:  :      |    ||    |             :   :: :   |:||   :
Db        506 SYVYNGYSVVFVGTKSGKLKKIRADGPP------------HGGVQYEMVSVLKDGSPIL 552

Qy        120 TTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVF-PCLSIPCKLQSGTHCLWTDQLLQGS 178
                :|      | :   |  |:     ||: |   |||          || |
Db        553 RDMAFSIDQRYLYVMSERQVTRVPVESCEQYTTCGECLS-----SGDPHCGWC------- 600

Qy        179 EKGFQSRHLACLPREPGLCTWQSLR 203
                 : |  |  |:     |:  |
Db        601 -----ALHNMCSRRDKCQQAWEPNR 620


RESULT 15
US-11-098-686-10425
; Sequence 10425, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10425
;   LENGTH: 304
```

```
;   TYPE: PRT
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-10425

  Query Match             7.2%;  Score 80.5;  DB 7;  Length 304;
  Best Local Similarity   24.0%;  Pred. No. 0.49;
  Matches   49;  Conservative   21;  Mismatches   67;  Indels   67;  Gaps   11;

Qy          2 APFEPLASGILLLLWLIAPSRACTCVPPHPQTAFC--NSDLVI--RAKFVGTPEVNQ-TT 56
              ||| |: :| |       |  :|   || |    |  |   |:  | : ||: :  |
Db         24 APFRPVPAGKL-------PPVSC---PPVPGLFQCSRNGSAVVARRRQHVGSGKKKQGGK 73

Qy         57 LYQRYEIKMTKMYKGFQALGDAADIRFVY----TPAMESVCGYFHRSHNRSEEFLIAGKL 112
               |:|                    ||: |      |:: :| |   |     : : : |::
Db         74 SYER-----------------DIKTVIPGTGEPSVRTVYGSCERKAEYGQSYPLVGRI 114

Qy        113 QDGLLHITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTD 172
                |:| |           || |                 ||  |    | |
Db        115 GQ-LIHAT----------GLAGRGK--------------PCRQIRTLFQKGPGSAKLF 147

Qy        173 QLLQGSEKGFQSRHLACLPREPGL 196
              | | |  :| :  |: || |  ||
Db        148 QTLLG--RGRKLLHIPCLFRRSGL 169


Search completed: April 10, 2006, 18:13:21
Job time : 8.51485 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:34 ; Search time 70.1386 Seconds
(without alignments)
2082.225 Million cell updates/sec

Title: US-10-734-564-100
Perfect score: 1124
Sequence: 1 MAPFEPLASGILLLLWLIAP.....ACLPREPGLCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1124	100.0	207	1	TIMP1_HUMAN	P01033 homo sapien
2	1124	100.0	207	2	Q6FGX5_HUMAN	Q6fgx5 homo sapien
3	1124	100.0	207	2	Q5RC60_PONPY	Q5rc60 pongo pygma
4	1117	99.4	207	1	TIMP1_PAPCY	P49061 papio cynoc
5	1104	98.2	207	1	TIMP1_MACMU	Q95kl9 macaca mula
6	1000.5	89.0	188	2	Q58P21_HUMAN	Q58p21 homo sapien
7	995	88.5	207	1	TIMP1_BOVIN	P20414 bos taurus
8	967	86.0	207	1	TIMP1_PIG	P35624 sus scrofa
9	961	85.5	207	1	TIMP1_SHEEP	P50122 ovis aries
10	926	82.4	207	1	TIMP1_HORSE	O02722 equus cabal
11	925	82.3	207	2	Q5ENG6_RABIT	Q5eng6 oryctolagus
12	915	81.4	169	2	Q96QM2_HUMAN	Q96qm2 homo sapien
13	911	81.0	203	2	Q5ENG7_RABIT	Q5eng7 oryctolagus
14	903	80.3	207	1	TIMP1_CANFA	P81546 canis famil
15	902.5	80.3	206	1	TIMP1_RABIT	P20614 oryctolagus
16	837.5	74.5	205	1	TIMP1_MOUSE	P12032 mus musculu
17	818	72.8	217	1	TIMP1_RAT	P30120 rattus norv
18	818	72.8	217	2	Q53YM7_RAT	Q53ym7 rattus norv
19	782	69.6	143	2	Q5H9A7_HUMAN	Q5h9a7 homo sapien
20	633	56.3	137	2	Q9MZ12_SHEEP	Q9mz12 ovis aries
21	588	52.3	136	2	Q5H9B5_HUMAN	Q5h9b5 homo sapien
22	543	48.3	164	2	Q5H9A8_HUMAN	Q5h9a8 homo sapien
23	515	45.8	145	2	Q91ZP7_RAT	Q91zp7 rattus norv
24	505	44.9	114	2	Q6QLW9_CANFA	Q6qlw9 canis famil
25	446	39.7	108	2	Q6X809_FELCA	Q6x809 felis silve
26	444	39.5	96	2	Q5H9B4_HUMAN	Q5h9b4 homo sapien
27	420.5	37.4	220	1	TIMP2_MOUSE	P25785 mus musculu
28	420.5	37.4	220	1	TIMP2_RAT	P30121 rattus norv
29	420.5	37.4	220	2	Q546J4_RAT	Q546j4 rattus norv
30	420.5	37.4	220	2	Q6PI17_MOUSE	Q6pi17 mus musculu
31	416.5	37.1	220	2	Q8BSJ3_MOUSE	Q8bsj3 mus musculu
32	415.5	37.0	220	1	TIMP2_HUMAN	P16035 homo sapien
33	407.5	36.3	220	1	TIMP2_CANFA	Q9tty1 canis famil
34	406	36.1	222	2	Q5FVZ1_XENTR	Q5fvz1 xenopus tro
35	406	36.1	222	2	Q66IW0_XENLA	Q66iw0 xenopus lae
36	401.5	35.7	220	1	TIMP2_CAVPO	Q9wuc6 cavia porce
37	401	35.7	220	1	TIMP2_CHICK	O42146 gallus gall
38	398.5	35.5	214	1	TIMP3_SCYTO	Q9w6b4 scyliorhinu
39	398	35.4	220	2	Q64HW8_ONCMY	Q64hw8 oncorhynchu
40	397	35.3	220	2	Q4W7T6_ORYLA	Q4w7t6 oryzias lat
41	397	35.3	220	2	Q4JF85_FUGRU	Q4jf85 fugu rubrip
42	396.5	35.3	100	2	Q6GXA9_MOUSE	Q6gxa9 mus musculu
43	395	35.1	220	2	Q60FR5_PAGMA	Q60fr5 pagrus majo
44	394.5	35.1	220	1	TIMP2_BOVIN	P16368 bos taurus
45	393	35.0	220	2	Q6GLM1_XENLA	Q6glm1 xenopus lae

ALIGNMENTS

RESULT 1
TIMP1_HUMAN
ID TIMP1_HUMAN STANDARD; PRT; 207 AA.
AC P01033; Q14252; Q9UCU1;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid
DE potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases)
DE (Fibroblast collagenase inhibitor) (Collagenase inhibitor).
GN Name=TIMP1; Synonyms=CLGI, TIMP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86040463; PubMed=3903517;
RA Docherty A.J.P., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,
RA Harris T.J.R., Murphy G., Reynolds J.J.;
RT "Sequence of human tissue inhibitor of metalloproteinases and its
RT identity to erythroid-potentiating activity.";
RL Nature 318:66-69(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85240567; PubMed=3839290;
RA Gasson J.C., Golde D.W., Kaufman S.E., Westbrook C.A., Hewick R.M.,
RA Kaufman R.J., Wong G.G., Temple P.A., Leary A.C., Brown E.L.,
RA Orr E.C., Clark S.C.;
RT "Molecular characterization and expression of the gene encoding human
RT erythroid-potentiating activity.";
RL Nature 315:768-771(1985).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=86205964; PubMed=3010309;
RA Carmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,
RA Welgus H.G., Stricklin G.P.;
RT "Primary structure and cDNA cloning of human fibroblast collagenase
RT inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411(1986).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kaczorek M., Honore N., Ribes V., Dehoux P., Cornet P., Cartwright T.,
RA Streeck R.E.;
RT "Molecular cloning and synthesis of biologically active human tissue
RT inhibitor of metalloproteinases in yeast.";
RL Biotechnology (N.Y.) 5:595-598(1987).
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Ovary;
RX MEDLINE=91025550; PubMed=2171551;
RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
RA Scheit K.H.;

```
RT   "Characterization of three abundant mRNAs from human ovarian granulosa
RT   cells.";
RL   DNA Cell Biol. 9:479-485(1990).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94123576; PubMed=7507419;
RA   Opbroek A., Kenney M.C., Brown D.;
RT   "Characterization of a human corneal metalloproteinase inhibitor
RT , (TIMP-1).";
RL   Curr. Eye Res. 12:877-883(1993).
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Cervix;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   NUCLEOTIDE SEQUENCE OF 42-207.
RA   Matsuda T., Kohno K., Kuwano M.;
RL   Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   NUCLEOTIDE SEQUENCE OF 1-40.
RA   Hardcastle A.J.;
RL   Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   DISULFIDE BONDS, AND PARTIAL PROTEIN SEQUENCE.
RX   MEDLINE=90303199; PubMed=2163605;
RA   Williamson R.A., Martson F.A.O., Angal S., Koklitis P., Panico M.,
RA   Morris H.R., Carne A.F., Smith B.J., Harris T.J.R., Freedman R.B.;
RT   "Disulphide bond assignment in human tissue inhibitor of
RT   metalloproteinases (TIMP).";
RL   Biochem. J. 268:267-274(1990).
RN   [11]
RP   PROTEIN SEQUENCE OF 24-38.
RC   TISSUE=Synovial fluid;
RX   MEDLINE=92111776; PubMed=1730286; DOI=10.1016/0014-5793(92)80393-U;
RA   Osthues A., Knaueper V., Oberhoff R., Reinke H., Tschesche H.;
RT   "Isolation and characterization of tissue inhibitors of
RT   metalloproteinases (TIMP-1 and TIMP-2) from human rheumatoid synovial
RT   fluid.";
RL   FEBS Lett. 296:16-20(1992).
RN   [12]
RP   PROTEIN SEQUENCE OF 24-52.
RX   MEDLINE=91355647; PubMed=1653055; DOI=10.1016/1043-4666(91)90021-5;
RA   van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,
RA   Auwerx J., van Damme J., Opdenakker G.;
RT   "The cytokine-protease connection: identification of a 96-kD THP-1
RT   gelatinase and regulation by interleukin-1 and cytokine inducers.";
RL   Cytokine 3:231-239(1991).
RN   [13]
RP   PROTEIN SEQUENCE OF 24-38.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [14]
RP   MUTAGENESIS.
RX   MEDLINE=93041700; PubMed=1420137;
RA   O'Shea M., Willenbrock F., Williamson R.A., Cockett M.I.,
RA   Freedman R.B., Reynolds J.J., Docherty A.J.P., Murphy G.;
RT   "Site-directed mutations that alter the inhibitory activity of the
RT   tissue inhibitor of metalloproteinases-1: importance of the N-terminal
RT   region between cysteine 3 and cysteine 13.";
RL   Biochemistry 31:10146-10152(1992).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH MMP-3.
RX   MEDLINE=97433330; PubMed=9288970; DOI=10.1038/37995;
RA   Gomis-Rueth F.-X., Maskos K., Betz M., Bergner A., Huber R.,
RA   Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P.,
RA   Bartunik H., Bode W.;
RT   "Mechanism of inhibition of the human matrix metalloproteinase
RT   stromelysin-1 by TIMP-1.";
RL   Nature 389:77-81(1997).
RN   [16]
RP   STRUCTURE BY NMR OF 24-149.
RX   MEDLINE=20090931; PubMed=10623524; DOI=10.1006/jmbi.1999.3362;
RA   Wu B., Arumugam S., Gao G., Lee G.I., Semenchenko V., Huang W.,
RA   Brew K., Van Doren S.R.;
RT   "NMR structure of tissue inhibitor of metalloproteinases-1 implicates
RT   localized induced fit in recognition of matrix metalloproteinases.";
RL   J. Mol. Biol. 295:257-268(2000).
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them. Also mediates erythropoiesis in
CC       vitro; but, unlike IL-3, it is species-specific, stimulating the
CC       growth and differentiation of only human and murine erythroid
CC       progenitors. Known to act on MMP-1, MMP-2, MMP-3, MMP-7, MMP-8,
CC       MMP-9, MMP-10, MMP-11, MMP-12, MMP-13 and MMP-16. Does not act on
CC       MMP-14.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X03124; CAA26902.1; -; mRNA.
DR   EMBL; M12670; AAA52436.1; -; mRNA.
DR   EMBL; X02598; CAA26443.1; -; mRNA.
DR   EMBL; M59906; AAA63234.1; -; mRNA.
DR   EMBL; S68252; AAD14009.1; -; mRNA.
DR   EMBL; BC000866; AAH00866.1; -; mRNA.
DR   EMBL; D11139; BAA01913.1; -; Genomic_DNA.
DR   EMBL; L47361; AAA75558.1; -; Genomic_DNA.
DR   EMBL; A10416; CAA00898.1; -; Unassigned_RNA.
DR   PIR; A93372; ZYHUEP.
DR   PDB; 1D2B; NMR; A=24-149.
DR   PDB; 1LQN; Model; A=1-207.
DR   PDB; 1OO9; NMR; B=24-149.
DR   PDB; 1UEA; X-ray; B/D=24-207.
DR   GlycoSuiteDB; P01033; -.
DR   Ensembl; ENSG00000102265; Homo sapiens.
DR   HGNC; HGNC:11820; TIMP1.
DR   H-InvDB; HIX0016764; -.
DR   MIM; 305370; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IDA.
DR   GO; GO:0051045; P:negative regulation of membrane protein ect. . .; IDA.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_Inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
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DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.

  Query Match             100.0%;  Score 1124;  DB 1;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-104;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
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Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 2
Q6FGX5_HUMAN
ID   Q6FGX5_HUMAN PRELIMINARY;      PRT;   207 AA.
AC   Q6FGX5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   TIMP1 protein (Tissue inhibitor of metalloproteinase 1) (Erythroid
DE   potentiating activity, collagenase inhibitor).
GN   Name=TIMP1; ORFNames=RP1-230G1.3-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT   "Cloning of human full open reading frames in Gateway(TM) system entry
RT   vector (pDONR201).";
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Wray P.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR541982; CAG46779.1; -; mRNA.
DR   EMBL; CR407638; CAG28566.1; -; mRNA.
DR   EMBL; Z84466; CAI42465.1; -; Genomic_DNA.
DR   SMR; Q6FGX5; 24-204.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   Pfam; PF00965; TIMP; 1.
DR   SMART; SM00206; NTR; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Collagen.
SQ   SEQUENCE   207 AA;  23171 MW;  5AE4F90FFAB2ECDC CRC64;

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-104;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
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Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 3
Q5RC60_PONPY
ID   Q5RC60_PONPY PRELIMINARY;      PRT;   207 AA.
AC   Q5RC60;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp468A0912.
GN   Name=DKFZp468A0912;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RG   The German cDNA Consortium;
RA   Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR858421; CAH90650.1; -; mRNA.
DR   SMR; Q5RC60; 24-204.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   SMART; SM00206; NTR; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   207 AA;  23171 MW;  5AE4F90FFAB2ECDC CRC64;

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-104;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

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RESULT 4
TIMP1_PAPCY
ID   TIMP1_PAPCY    STANDARD;      PRT;   207 AA.
AC   P49061;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   Name=TIMP1;
OS   Papio cynocephalus (Yellow baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9556;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Aorta;
RX   MEDLINE=96011646; PubMed=7590279; DOI=10.1016/0378-1119(95)00343-5;
RA   Forough R., Nikkari S.T., Hasenstab D., Lea H., Clowes A.W.;
RT   "Cloning and characterization of a cDNA encoding the baboon tissue
RT   inhibitor of matrix metalloproteinase-1 (TIMP-1).";
RL   Gene 163:267-271(1995).
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; L37295; AAA99943.1; -; mRNA.
DR   HSSP; P01033; 1OO9.
DR   SMR; P49061; 24-204.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW   Metalloprotease inhibitor; Signal.
FT   SIGNAL        1     23       By similarity.
FT   CHAIN        24    207       Metalloproteinase inhibitor 1.
FT   DOMAIN       24    147       NTR.
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     24     93       By similarity.
FT   DISULFID     26    122       By similarity.
FT   DISULFID     36    147       By similarity.
FT   DISULFID    150    197       By similarity.
FT   DISULFID    155    160       By similarity.
FT   DISULFID    168    189       By similarity.
SQ   SEQUENCE   207 AA;  23213 MW;  5AE4FBDBEAB2ECDC CRC64;

  Query Match             99.4%;  Score 1117;  DB 1;  Length 207;
  Best Local Similarity   99.0%;  Pred. No. 2.8e-103;
  Matches  205;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||::||
Db        181 GFQSRHLACLPREPGLCTWQSLRTRIA 207


RESULT 5
TIMP1_MACMU
ID   TIMP1_MACMU    STANDARD;      PRT;   207 AA.
AC   Q95KL9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   Name=TIMP1;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RA   Ji S., Wang Y., Li H., Ji W., Piao Y.;
RT   "Cloning and characterization of tissue inhibitor of matrix
RT   metalloproteinase-1 (TIMP-1) cDNA from Macaca mulatta.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF366397; AAK53704.1; -; mRNA.
DR   HSSP; P01033; 1OO9.
DR   SMR; Q95KL9; 24-204.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; FALSE_NEG.
KW   Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW   Metalloprotease inhibitor; Signal.
FT   SIGNAL        1     23       By similarity.
FT   CHAIN        24    207       Metalloproteinase inhibitor 1.
FT   DOMAIN       24    147       NTR.
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     24     93       By similarity.
FT   DISULFID     26    122       By similarity.
FT   DISULFID     36    147       By similarity.
FT   DISULFID    150    197       By similarity.
FT   DISULFID    155    160       By similarity.
FT   DISULFID    168    189       By similarity.
SQ   SEQUENCE   207 AA;  23247 MW;  46E227D2AABBA580 CRC64;

  Query Match             98.2%;  Score 1104;  DB 1;  Length 207;
  Best Local Similarity   98.1%;  Pred. No. 5.5e-102;
  Matches  203;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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                  |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVLPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
                  |||||||||||||||||||:::|
Db        181 GFQSRHLACLPREPGLCTWQSLRTRMA 207


RESULT 6
Q58P21_HUMAN
ID   Q58P21_HUMAN PRELIMINARY;      PRT;   188 AA.
AC   Q58P21;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Tissue inhibitor of metalloproteinase 1 (Fragment).
GN   Name=TIMP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22383613; PubMed=12496489;
RA   Wang M., Hu Y., Shima I., Stearns M.E.;
RT   "IL-10/IL-10 receptor signaling regulates TIMP-1 expression in primary
RT   human prostate tumor lines.";
RL   Cancer Biol. Ther. 1:556-563(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98451715; PubMed=9778693;
RA   Wang M., Hu Y., Shima I., Stearns M.E.;
RT   "Identification of positive and negative regulator elements for the
RT   tissue inhibitor of metalloproteinase 1 gene.";
RL   Oncol. Res. 10:219-233(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Wang M., Hu Y., Stearns M.E.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY932824; AAX47478.1; -; Genomic_DNA.
DR   SMR; Q58P21; 24-187.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   Pfam; PF00965; TIMP; 1.
DR   SMART; SM00206; NTR; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
FT   NON_TER     188    188
SQ   SEQUENCE   188 AA;  20917 MW;  DCD275A33ADB6AC7 CRC64;

  Query Match             89.0%;  Score 1000.5;  DB 2;  Length 188;
  Best Local Similarity   97.9%;  Pred. No. 1.1e-91;
  Matches  186;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||   :|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YE---SKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 117

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 177

Qy        181 GFQSRHLACL 190
              ||||||||||
Db        178 GFQSRHLACL 187


RESULT 7
TIMP1_BOVIN
ID   TIMP1_BOVIN    STANDARD;      PRT;   207 AA.
AC   P20414; Q53ZP2; Q9TVB0;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-
DE   1).
GN   Name=TIMP1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=90365711; PubMed=2393392;
RA   Freudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.;
RT   "mRNA of bovine tissue inhibitor of metalloproteinase: sequence and
RT   expression in bovine ovarian tissue.";
RL   Biochem. Biophys. Res. Commun. 171:250-256(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=94257757; PubMed=8199264;
RA   Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;
RT   "Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa
RT   and oviduct cells enhances in vitro development of bovine embryo.";
RL   Biol. Reprod. 50:835-844(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Adrenal cortex;
RA   Reichenstein M., Reich R., Lehoux J.-G., Hanukoglu I.;
RT   "ACTH induces TIMP-1 expression and inhibits collagenase in adrenal
RT   cortex cells.";
RL   Mol. Cell. Endocrinol. 215:109-114(2004).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 25-191.
RC   TISSUE=Skeletal muscle;
RA   Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.;
RT   "Involvement of fibroblasts and muscle cells in the expression of an
RT   extracellular proteolytic cascade in bovine skeletal muscle.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   PRELIMINARY PROTEIN SEQUENCE OF 24-69.
RX   MEDLINE=90008914; PubMed=2551903;
RA   de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;
RT   "Purification and characterization of two related but distinct
RT   metalloproteinase inhibitors secreted by bovine aortic endothelial
RT   cells.";
RL   J. Biol. Chem. 264:17445-17453(1989).
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
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CC   ----------------------------------------------------------------------
DR   EMBL; M60073; AAA30784.1; -; mRNA.
DR   EMBL; S70841; AAB30892.1; -; mRNA.
DR   EMBL; AY295346; AAP44413.1; -; mRNA.
DR   EMBL; AF144763; AAD30303.1; -; mRNA.
DR   PIR; A35685; A35685.
DR   HSSP; P01033; 1UEA.
DR   SMR; P20414; 24-204.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Direct protein sequencing; Erythrocyte maturation; Glycoprotein;
KW   Metalloenzyme inhibitor; Metalloprotease inhibitor; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    207       Metalloproteinase inhibitor 1.
FT   DOMAIN       24    147       NTR.
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     24     93       By similarity.
FT   DISULFID     26    122       By similarity.
FT   DISULFID     36    147       By similarity.
FT   DISULFID    150    197       By similarity.
FT   DISULFID    155    160       By similarity.
FT   DISULFID    168    189       By similarity.
SQ   SEQUENCE   207 AA;  23032 MW;  E672BEE2E865F3F7 CRC64;

  Query Match             88.5%;  Score 995;  DB 1;  Length 207;
  Best Local Similarity   87.0%;  Pred. No. 4.4e-91;
  Matches  180;  Conservative   11;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||| |:|||||||||| ||||||||||||||||||||:||||||||| |||:| ||||
Db          1 MAPFAPMASGILLLLWLTAPSRACTCVPPHPQTAFCNSDVVIRAKFVGTAEVNETALYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||:||| || || |||:|||||||||||||| ||||||||||:| :| ||||
Db         61 YEIKMTKMFKGFSALRDAPDIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQLSNGHLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||:| |||||||||  |||||||||| |||||||| |||||||||| ||:|
Db        121 TCSFVAPWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||:|:|
Db        181 GFQSRHLACLPREPGLCTWQSLRAQMA 207


RESULT 8
TIMP1_PIG
ID   TIMP1_PIG      STANDARD;      PRT;   207 AA.
AC   P35624; Q9TT83; Q9TTB9;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   Name=TIMP1;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Ovary;
RX   MEDLINE=92201478; PubMed=1312961; DOI=10.1016/0303-7207(92)90196-D;
RA   Tanaka T., Andoh N., Takeya T., Sato E.;
RT   "Differential screening of ovarian cDNA libraries detected the
RT   expression of the porcine collagenase inhibitor gene in functional
RT   corpora lutea.";
RL   Mol. Cell. Endocrinol. 83:65-71(1992).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 34-195.
RA   Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
RT   "Gene expression level of mmp3 and Timp1 in intervertebral disc.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 37-144.
RC   TISSUE=Skin;
RA   Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
RT   "Cloning and sequencing of porcine TIMPs.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; S96211; AAB21865.1; -; mRNA.
DR   EMBL; AF201726; AAF24348.1; -; mRNA.
DR   EMBL; AF156029; AAF17354.1; -; mRNA.
DR   PIR; I47061; I47061.
DR   HSSP; P01033; 1UEA.
DR   SMR; P35624; 24-203.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW   Metalloprotease inhibitor; Signal.
FT   SIGNAL        1     23       By similarity.
FT   CHAIN        24    207       Metalloproteinase inhibitor 1.
FT   DOMAIN       24    147       NTR.
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     24     93       By similarity.
FT   DISULFID     26    122       By similarity.
FT   DISULFID     36    147       By similarity.
FT   DISULFID    150    197       By similarity.
FT   DISULFID    155    160       By similarity.
FT   DISULFID    168    189       By similarity.
FT   CONFLICT     34     34       A -> P (in Ref. 2).
FT   CONFLICT     37     37       S -> N (in Ref. 3).
FT   CONFLICT     41     41       V -> F (in Ref. 2).
FT   CONFLICT     59     59       K -> Q (in Ref. 1).
FT   CONFLICT     86     86       T -> A (in Ref. 3).
FT   CONFLICT    141    142       EI -> KT (in Ref. 3).
SQ   SEQUENCE   207 AA;  23099 MW;  B04895846EB56BD0 CRC64;

  Query Match             86.0%;  Score 967;  DB 1;  Length 207;
  Best Local Similarity   83.6%;  Pred. No. 2.8e-88;
  Matches  173;  Conservative   15;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |:|| |||||||||||| ||||||||||||||||:|||||||||| || |||  |:|
Db          1 MSPFAPLASGILLLLWLTAPSRACTCVPPHPQTAFCSSDLVIRAKFVGAPEFNQTASYKR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||:||| |||| |||||:|||||||||||||| |||:|||||||:| :| ||||
Db         61 YEIKMTKMFKGFNALGDAPDIRFIYTPAMESVCGYFHRSQNRSQEFLIAGQLWNGHLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              |||||||||||| |||:|||: |  |||||||||| |||||||| |||||||||| ||:|
Db        121 TCSFVAPWNSLSSAQRQGFTEIYAAGCEECTVFPCTSIPCKLQSDTHCLWTDQLLTGSDK 180
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Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||:|||||:||||||| ::|
Db        181 GFQSRHLACMPREPGMCTWQSLRPRVA 207


RESULT 9
TIMP1_SHEEP
ID   TIMP1_SHEEP    STANDARD;      PRT;   207 AA.
AC   P50122;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   Name=TIMP1;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Corpus luteum;
RX   MEDLINE=94102210; PubMed=8275949; DOI=10.1210/en.134.1.344;
RA   Smith G.W., Goetz T.L., Anthony R.V., Smith M.F.;
RT   "Molecular cloning of an ovine ovarian tissue inhibitor of
RT   metalloproteinases: ontogeny of messenger ribonucleic acid expression
RT   and in situ localization within preovulatory follicles and luteal
RT   tissue.";
RL   Endocrinology 134:344-352(1994).
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; S67450; AAB29472.1; -; mRNA.
DR   PIR; I46964; I46964.
DR   HSSP; P01033; 1UEA.
DR   SMR; P50122; 24-203.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW   Metalloprotease inhibitor; Signal.
FT   SIGNAL        1     23       By similarity.
FT   CHAIN        24    207       Metalloproteinase inhibitor 1.
FT   DOMAIN       24    147       NTR.
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     24     93       By similarity.
FT   DISULFID     26    122       By similarity.
FT   DISULFID     36    147       By similarity.
FT   DISULFID    150    197       By similarity.
FT   DISULFID    155    160       By similarity.
FT   DISULFID    168    189       By similarity.
SQ   SEQUENCE   207 AA;  23058 MW;  1D3BCA2012F80E46 CRC64;

  Query Match             85.5%;  Score 961;  DB 1;  Length 207;
  Best Local Similarity   85.7%;  Pred. No. 1.1e-87;
  Matches  174;  Conservative   10;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              || | |  |||||||| ||||||||||||||||||::||||||||| |||:| ||||
Db          1 MALFAPTVSGILLLLWLTAPSRACTCVPPHPQTAFCNSEVVIRAKFVGTAEVNETALYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |||||||:||| || || ||||:|||||||||||||| ||||||||||:| :| ||||
Db         61 YEIKMTKMFKGFSALRDAPDIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQLSNGHLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||:| |||||||||  |||||||||| |||||||| |||||||||| ||:|
Db        121 TCSFVAPWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLR 203
              |||||||||||||||:|||||||
Db        181 GFQSRHLACLPREPGMCTWQSLR 203


RESULT 10
TIMP1_HORSE
ID   TIMP1_HORSE    STANDARD;      PRT;   207 AA.
AC   O02722;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   Name=TIMP1;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Cartilage;
RX   MEDLINE=99074117; PubMed=9858406;
RA   Richardson D.W., Dodge G.R.;
RT   "Molecular characteristics of equine stromelysin and the tissue
RT   inhibitor of metalloproteinase 1.";
RL   Am. J. Vet. Res. 59:1557-1562(1998).
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds (By similarity).
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; U95039; AAB53735.1; -; mRNA.
DR   HSSP; P01033; 1UEA.
DR   SMR; O02722; 24-203.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW   Metalloprotease inhibitor; Signal.
FT   SIGNAL        1     23       By similarity.
FT   CHAIN        24    207       Metalloproteinase inhibitor 1.
FT   DOMAIN       24    147       NTR.
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     24     93       By similarity.
FT   DISULFID     26    122       By similarity.
FT   DISULFID     36    147       By similarity.
FT   DISULFID    150    197       By similarity.
FT   DISULFID    155    160       By similarity.
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FT   DISULFID    168    189       By similarity.
SQ   SEQUENCE   207 AA;  23046 MW;  FD710DA98D168070 CRC64;

  Query Match             82.4%;  Score 926;  DB 1;  Length 207;
  Best Local Similarity   82.6%;  Pred. No. 3.5e-84;
  Matches  171;  Conservative   12;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||| || |||||||| |||||||||||||||||:|: |||||||| ||||||| :|
Db          1 MAPFAPLVSGILLLLWLTAPSRACTCVPPHPQTAFCSSEFVIRAKFVGTSEVNQTTLQRR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||:||| ||||| |  |||||||||:||||||| ||||||||||:| |  |:||
Db         61 YEIKMTKMFKGFSALGDAPDTWFVYTPAMESLCGYFHRSENRSEEFLIAGQLLDEKLYIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              |||||||||||| |||:|||||  || ||:|||| |||||||| | |||||||| ||:|
Db        121 TCSFVAPWNSLSSAQRQGFTKTYAAGCGECSVFPCSSIPCKLQSDTDCLWTDQLLTGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||:||||||||||||||| : |
Db        181 GFQSRYLACLPREPGLCTWQSLRPRTA 207


RESULT 11
Q5ENG6_RABIT
ID   Q5ENG6_RABIT PRELIMINARY;      PRT;   207 AA.
AC   Q5ENG6;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Tissue inhibitor of metalloproteinase 1.
GN   Name=TIMP-1;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Estelle J., Sastre Y., Merchan M., Folch J.M.;
RT   "Characterization and sequencing of the rabbit TIMP-1 gene.";
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY829731; AAW79054.1; -; Genomic_DNA.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   Pfam; PF00965; TIMP; 1.
DR   SMART; SM00206; NTR; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
SQ   SEQUENCE   207 AA;  22937 MW;  FA39B19352370B5B CRC64;

  Query Match             82.3%;  Score 925;  DB 2;  Length 207;
  Best Local Similarity   82.3%;  Pred. No. 4.4e-84;
  Matches  167;  Conservative   12;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||   ||| :||||||:|||||||||||||||||||||||||||| |||| ||||||
Db          1 MAPLAALASSMLLLLWLVAPSRACTCVPPHPQTAFCNSDLVIRAKFVGAPEVNHTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |||| |||:||| ||| | |||||||||||||||| |:| ||||||||||:|::||||||
Db         61 YEIKTTKMFKGFDALGHATDIRFVYTPAMESVCGYSHKSQNRSEEFLIAGQLRNGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||| |||||| :|| |||||| ||: |||| | |||| |:| |||||||||| ||:|
Db        121 TCSFVVPWNSLSFSQRSGFTKTYAAGCDMCTVFACASIPCHLESDTHCLWTDQLLLGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLR 203
              ||||||||||:||||| |||||
Db        181 GFQSRHLACLPQEPGLCAWQSLR 203


RESULT 12
Q96QM2_HUMAN
ID   Q96QM2_HUMAN PRELIMINARY;      PRT;   169 AA.
AC   Q96QM2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   TIMP1 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC007097; AAH07097.1; -; mRNA.
DR   HSSP; P01033; 1OO9.
DR   SMR; Q96QM2; 24-169.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR   GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   SMART; SM00206; NTR; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
SQ   SEQUENCE   169 AA;  18847 MW;  6C164206C87D815C CRC64;

  Query Match             81.4%;  Score 915;  DB 2;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-83;
  Matches  169;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCL 169
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCL 169
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RESULT 13
Q5ENG7_RABIT
ID   Q5ENG7_RABIT PRELIMINARY;      PRT;   203 AA.
AC   Q5ENG7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Tissue inhibitor of metalloproteinase 1 (Fragment).
GN   Name=TIMP-1;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Estelle J., Sastre Y., Merchan M., Folch J.M.;
RT   "Characterization and sequencing of the rabbit TIMP-1 gene.";
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY829730; AAW79053.1; -; mRNA.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   Pfam; PF00965; TIMP; 1.
DR   SMART; SM00206; NTR; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   203 AA;  22525 MW;  E1D1CE13047AEEF5 CRC64;

  Query Match             81.0%;  Score 911;  DB 2;  Length 203;
  Best Local Similarity   83.2%;  Pred. No. 1.1e-82;
  Matches  164;  Conservative   12;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          7 LASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMT 66
              ||| :||||||:||||||||||||||||||||||||||||| |||| |||||||||| |
Db          3 LASSMLLLLWLVAPSRACTCVPPHPQTAFCNSDLVIRAKFVGAPEVNHTTLYQRYEIKTT 62

Qy         67 KMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTCSFVA 126
              ||:||| ||| | |||||||||||||||| |:| ||||||||||:|::||||||||||
Db         63 KMFKGFDALGHATDIRFVYTPAMESVCGYSHKSQNRSEEFLIAGQLRNGLLHITTCSFVV 122

Qy        127 PWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQSRH 186
              |||||| :|| |||||| ||: |||| | |||| |:| |||||||||| ||:|||||||
Db        123 PWNSLSFSQRSGFTKTYAAGCDMCTVFACASIPCHLESDTHCLWTDQLLLGSDKGFQSRH 182

Qy        187 LACLPREPGLCTWQSLR 203
              |||||:||||| |||||
Db        183 LACLPQEPGLCAWQSLR 199


RESULT 14
TIMP1_CANFA
ID   TIMP1_CANFA    STANDARD;      PRT;   207 AA.
AC   P81546; Q9TQS5;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   Name=TIMP1;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Cocker spaniel; TISSUE=Kidney;
RA   Noritake H., Miyamori H., Goto C., Seiki M., Sato H.;
RT   "Overexpression of tissue inhibitor of matrix metalloproteinases-1
RT   (TIMP-1) in metastatic MDCK cells transformed by v-src.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99132652; PubMed=9931441; DOI=10.1016/S0378-1119(98)00521-6;
RA   Zeiss C.J., Acland G.M., Aguirre G.D., Ray K.;
RT   "TIMP-1 expression is increased in X-linked progressive retinal
RT   atrophy despite its exclusion as a candidate gene.";
RL   Gene 225:67-75(1998).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=92175241; PubMed=1794505;
RA   Chopra R., Koklitis P.A., Bergin S., Rowe J., Angal S.;
RT   "Purification of recombinant dog tissue inhibitor of
RT   metalloproteinases.";
RL   Biochem. Soc. Trans. 19:372S-372S(1991).
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed. Highest expression in
CC       kidney and ovary.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AB016817; BAA32393.1; -; mRNA.
DR   EMBL; AF077817; AAD10632.1; -; mRNA.
DR   EMBL; AF079767; AAD10633.1; -; Genomic_DNA.
DR   HSSP; P01033; 1UEA.
DR   SMR; P81546; 24-203.
DR   Ensembl; ENSCAFG00000015155; Canis familiaris.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; FALSE_NEG.
KW   Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW   Metalloprotease inhibitor; Signal.
FT   SIGNAL       1     23       By similarity.
FT   CHAIN       24    207       Metalloproteinase inhibitor 1.
FT   DOMAIN      24    147       NTR.
FT   CARBOHYD    53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    77     77       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    24     93       By similarity.
FT   DISULFID    26    122       By similarity.
FT   DISULFID    36    147       By similarity.
FT   DISULFID   150    197       By similarity.
FT   DISULFID   155    160       By similarity.
FT   DISULFID   168    189       By similarity.
FT   CONFLICT    17     17       V -> L (in Ref. 1).
FT   CONFLICT    35     35       L -> F (in Ref. 1).
FT   CONFLICT   173    173       H -> Q (in Ref. 1).
FT   CONFLICT   203    203       Missing (in Ref. 1).
SQ   SEQUENCE   207 AA;  22852 MW;  D36C8A67BB3B784D CRC64;

  Query Match             80.3%;  Score 903;  DB 1;  Length 207;
  Best Local Similarity   79.7%;  Pred. No. 6.9e-82;
  Matches  165;  Conservative   14;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||| |||| ||||||: |||||||| ||||||| ||| :||||||||| ||||| | :|
Db          1 MAPFAPLASCILLLLWVTAPSRACTCAPPHPQTALCNSQIVIRAKFVGTAEVNQTDLNRR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||:||| |||:|:||||| |||:|||||| ||| |||||||:|| |:|| | |
Db         61 YEIKMTKMFKGFSALGNASDIRFVDTPALESVCGYLHRSQNRSEEFLVAGNLRDGHLQIN 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
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```
                ||||||||:||| ||||||||||  ||| |||| | |||||||| |||||||  | ||:|
Db        121 TCSFVAPWSSLSTAQRRGFTKTYAAGCEGCTVFTCSSIPCKLQSDTHCLWTDHFLTGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||:|||||| ::|
Db        181 GFQSRHLACLPREPGICTWQSLRPRMA 207


RESULT 15
TIMP1_RABIT
ID   TIMP1_RABIT    STANDARD;      PRT;   206 AA.
AC   P20614;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN   Name=TIMP1;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89214135; PubMed=2708356;
RA   Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Notter R.H.,
RA   Quible D.J.;
RT   "Hyperoxic exposure alters gene expression in the lung. Induction of
RT   the tissue inhibitor of metalloproteinases mRNA and other mRNAs.";
RL   J. Biol. Chem. 264:7092-7095(1989).
CC   -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC       and irreversibly inactivates them.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: The activity of TIMP1 is dependent on the presence of
CC       disulfide bonds.
CC   -!- SIMILARITY: Belongs to the TIMP family.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; J04712; AAA31478.1; -; mRNA.
DR   PIR; A33350; A33350.
DR   HSSP; P01033; 1OO9.
DR   SMR; P20614; 24-202.
DR   InterPro; IPR001134; Netrin_C.
DR   InterPro; IPR001820; Prot_inh_TIMP.
DR   PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR   Pfam; PF00965; TIMP; 1.
DR   PROSITE; PS50189; NTR; 1.
DR   PROSITE; PS00288; TIMP; 1.
KW   Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW   Metalloprotease inhibitor; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    206       Metalloproteinase inhibitor 1.
FT   DOMAIN       24    147       NTR.
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    101    101       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     24     93       By similarity.
FT   DISULFID     26    122       By similarity.
FT   DISULFID     36    147       By similarity.
FT   DISULFID    150    196       By similarity.
FT   DISULFID    155    160       By similarity.
FT   DISULFID    168    188       By similarity.
SQ   SEQUENCE   206 AA;  22758 MW;  1839A8DE7174EE9E CRC64;

  Query Match             80.3%;  Score 902.5;  DB 1;  Length 206;
  Best Local Similarity   80.8%;  Pred. No. 7.7e-82;
  Matches  164;  Conservative   13;  Mismatches   25;  Indels    1;  Gaps    1;
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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||   ||| :||||||:||||||||||||||||||||||||||||| |||| ||||||
Db          1 MAPLAALASSMLLLLWLVAPSRACTCVPPHPQTAFCNSDLVIRAKFVGAPEVNHTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |||| |||:||| ||| | |||||||||||||||| |:| ||||||||||:|::||||||
Db         61 YEIKTTKMFKGFDALGHATDIRFVYTPAMESVCGYSHKSQNRSEEFLIAGQLRNGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||| |||||| :|| |||||| ||: |||| | |||| |:| |||||||  | ||:|
Db        121 TCSFVVPWNSLSFSQRSGFTKTYAAGCDMCTVFACASIPCHLESDTHCLWTDSSL-GSDK 179

Qy        181 GFQSRHLACLPREPGLCTWQSLR 203
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Db        180 GFQSRHLACLPQEPGLCAWESLR 202


Search completed: April 10, 2006, 18:06:34
Job time : 73.1386 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:01:46 ; Search time 11.8416 Seconds
(without alignments)
1681.943 Million cell updates/sec

Title: US-10-734-564-100
Perfect score: 1124
Sequence: 1 MAPFEPLASGILLLLWLIAP.....ACLPREPGLCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1124	100.0	207	1	ZYHUEP	metalloproteinase
2	1117	99.4	207	2	JC4303	matrix metalloprot
3	995	88.5	207	1	A35685	metalloproteinase
4	971	86.4	207	2	I47061	collagenase inhibi
5	961	85.5	207	2	I46964	metalloproteinase
6	902.5	80.3	206	1	A33350	metalloproteinase
7	837.5	74.5	205	1	A26106	metalloproteinase
8	818	72.8	217	1	JC2557	metalloproteinase
9	420.5	37.4	220	1	JH0683	metalloproteinase
10	420.5	37.4	220	2	I53415	tissue inhibitor o
11	417.5	37.1	220	1	S45683	metalloproteinase
12	415.5	37.0	220	1	A37128	metalloproteinase
13	394.5	35.1	220	1	A35996	metalloproteinase
14	389.5	34.7	211	1	S45317	metalloproteinase
15	388.5	34.6	196	1	S38624	metalloproteinase
16	388.5	34.6	212	1	A43429	metalloproteinase
17	385.5	34.3	211	1	A53532	metalloproteinase
18	384.5	34.2	211	2	JC4630	metalloproteinase
19	112.5	10.0	50	2	I53729	metalloproteinase
20	94	8.4	158	2	F89123	protein K07C11.5 [
21	86.5	7.7	433	1	B65058	fixC protein homol
22	86	7.7	461	1	GQRTT1	tumor necrosis fac
23	83	7.4	4307	2	T20721	hypothetical prote
24	82	7.3	454	1	GQMST1	tumor necrosis fac
25	81.5	7.3	1884	2	JC4975	plexin 2 precursor
26	78.5	7.0	433	2	E91081	hypothetical prote
27	78.5	7.0	433	2	F85926	hypothetical prote
28	78.5	7.0	724	2	G86271	protein F16A14.7 [
29	77.5	6.9	359	1	KIBEBT	thymidine kinase (
30	77.5	6.9	944	2	S66870	DNL4 protein - yea
31	76.5	6.8	183	2	A32851	22K extracellular
32	76.5	6.8	709	2	G96610	probable disease r
33	76	6.8	266	2	S02510	nifM protein - Kle
34	75.5	6.7	530	2	F84488	probable Ta11-like
35	75.5	6.7	1513	2	A54895	mucin 2, intestina
36	75	6.7	1356	2	JC1402	protein-tyrosine k
37	74.5	6.6	430	2	S73269	histidine-tRNA lig
38	74.5	6.6	444	2	S48696	suppressor protein
39	73.5	6.5	993	1	P1VXTA	RNA 1 protein - to
40	73	6.5	259	2	JC7109	ST2V protein - hum
41	73	6.5	480	2	F82796	hypothetical prote
42	73	6.5	537	2	I49135	prolyl 4-hydroxyla
43	73	6.5	555	2	D71444	probable thioester
44	72.5	6.5	611	2	A83926	hypothetical prote
45	72	6.4	589	2	G71462	probable ABC trans

ALIGNMENTS

RESULT 1
ZYHUEP
metalloproteinase tissue inhibitor 1 precursor [validated] - human
N;Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhib
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A93372; A93363; A23534; A20595; A35826; A48417; S20318; S15872; I52912; S
R;Docherty, A.J.P.; Lyons, A.; Smith, B.J.; Wright, E.M.; Stephens, P.E.; Harris, T.J.
Nature 318, 66-69, 1985
A;Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to
A;Reference number: A93372; MUID:86040463; PMID:3903517
A;Accession: A93372
A;Molecule type: mRNA
A;Residues: 1-207 <DOC>
A;Cross-references: UNIPROT:P01033; UNIPARC:UPI00001135B1; GB:X03124; NID:g37182; PIDN
R;Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.
Nature 315, 768-771, 1985
A;Title: Molecular characterization and expression of the gene encoding human erythroi
A;Reference number: A93363; MUID:85240567; PMID:3839290
A;Accession: A93363
A;Molecule type: mRNA
A;Residues: 1-207 <GAS>
A;Cross-references: UNIPARC:UPI00001135B1
R;Carmichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H
Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986
A;Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.
A;Reference number: A23534; MUID:86205964; PMID:3010309
A;Accession: A23534
A;Molecule type: mRNA
A;Residues: 1-207 <CAR>
A;Cross-references: UNIPARC:UPI00001135B1; GB:M12670; NID:g182482; PIDN:AAA52436.1; PI
A;Note: parts of this sequence were confirmed by protein sequencing
A;Note: carbohydrate binding sites were determined
R;Stricklin, G.P.; Welgus, H.G.
J. Biol. Chem. 258, 12252-12258, 1983
A;Title: Human skin fibroblast collagenase inhibitor.
A;Reference number: A20595; MUID:84032401; PMID:6313647
A;Accession: A20595
A;Molecule type: protein
A;Residues: 24-44,'L',46 <STR>
A;Cross-references: UNIPARC:UPI000002C59D
A;Note: six disulfide bonds are present
R;Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K
DNA Cell Biol. 9, 479-485, 1990
A;Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.
A;Reference number: A35826; MUID:91025550; PMID:2171551
A;Accession: A35826
A;Molecule type: mRNA
A;Residues: 1-207 <RAP>
A;Cross-references: UNIPARC:UPI00001135B1; GB:M38188
R;Van Ranst, M.; Norga, K.; Masure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van
Cytokine 3, 231-239, 1991

```
A;Title: The cytokine-protease connection: identification of a 96-kD THP-1 gelatinase an
A;Reference number: A48417; MUID:91355647; PMID:1653055
A;Accession: A48417
A;Molecule type: protein
A;Residues: 'X',25,'X',27-35,'X',37-52 <VAN>
A;Cross-references: UNIPARC:UPI0000173235
A;Experimental source: monocytic cell line THP-1
A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence incorrectly identified as 96K gelatinase
R;Osthues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.
FEBS Lett. 296, 16-20, 1992
A;Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP
A;Reference number: S20318; MUID:92111776; PMID:1730286
A;Accession: S20318
A;Molecule type: protein
A;Residues: 'X',25,'X',27-35,'X',37-38 <OST>
A;Cross-references: UNIPARC:UPI0000173236
A;Experimental source: rheumatoid synovial fluid
R;Opdenakker, G.; Masure, S.; Proost, P.; Billiau, A.; van Damme, J.
FEBS Lett. 284, 73-78, 1991
A;Title: Natural human monocyte gelatinase and its inhibitor.
A;Reference number: S15872; MUID:91285112; PMID:1647974
A;Accession: S15872
A;Molecule type: protein
A;Residues: 'X',25,'X',27-35,'X',37-42,'X',44,'X',46,'X',48-51 <FEB>
A;Cross-references: UNIPARC:UPI0000173237
A;Experimental source: peripheral blood monocytes
R;Williamson, R.A.; Marston, F.A.O.; Angal, S.; Koklitis, P.; Panico, M.; Morris, H.R.;
Biochem. J. 268, 267-274, 1990
A;Title: Disulphide bond assignment in human tissue inhibitor of metalloproteinases (TIM
A;Reference number: A38978; MUID:90303199; PMID:2163605
A;Contents: annotation; disulfide bonds
R;Opbroek, A.; Kenney, M.C.; Brown, D.
Curr. Eye Res. 12, 877-883, 1993
A;Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).
A;Reference number: I52912; MUID:94123576; PMID:7507419
A;Accession: I52912
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-207 <RES>
A;Cross-references: UNIPARC:UPI00001135B1; GB:S68252; NID:g545022; PIDN:AAD14009.1; PID:
R;Triebel, S.; Blaeser, J.; Gote, T.; Pelz, G.; Schueren, E.; Schmitt, M.; Tschesche, H.
Eur. J. Biochem. 231, 714-719, 1995
A;Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol
A;Reference number: S66461; MUID:95377303; PMID:7649172
A;Accession: S66461
A;Molecule type: protein
A;Residues: 24-38 <TRI>
A;Cross-references: UNIPARC:UPI0000173238
A;Experimental source: polymorphonuclear leukocytes
C;Comment: This protein, found in a variety of body fluids, complexes with metalloprotei
s-specific, stimulating the growth and differentiation of only human and murine erythroi
C;Comment: The remarkable heat stability of this protein may be due to disulfide bond fo
C;Genetics:
A;Gene: GDB:TIMP1; CLGI; TIMP
A;Cross-references: GDB:119615; OMIM:305370
A;Map position: Xp11.3-Xp11.23
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; glycoprotein; metalloproteinase inhibitor; mitogen
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F;24-93,26-122,36-147,150-197,155-160,168-189/Disulfide bonds: #status experimental
F;53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             100.0%;  Score 1124;  DB 1;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-101;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
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Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 2
JC4303
matrix metalloproteinase-1 tissue inhibitor - baboon
C;Species: Papio sp. (baboon)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 16-Jul-1999
C;Accession: JC4303
R;Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lea, H.; Clowes, A.W.
Gene 163, 267-271, 1995
A;Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of
A;Reference number: JC4303; MUID:96011646; PMID:7590279
A;Accession: JC4303
A;Molecule type: mRNA
A;Residues: 1-207 <FOR>
A;Cross-references: UNIPARC:UPI0000136F8E; GB:L37295; NID:g561545; PIDN:AAA99943.1; PID:
A;Experimental source: smooth muscle cell
C;Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase fa
se and influences the proteinase activity. It has a role as a physiological molecule for
C;Genetics:
A;Gene: timp-1
C;Superfamily: metalloproteinase inhibitor
C;Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F;53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             99.4%;  Score 1117;  DB 2;  Length 207;
  Best Local Similarity   99.0%;  Pred. No. 7.3e-101;
  Matches  205;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
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Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||::||
Db        181 GFQSRHLACLPREPGLCTWQSLRTRIA 207


RESULT 3
A35685
metalloproteinase inhibitor 1 precursor - bovine
N;Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhibi
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Sep-1990 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A35685; B34468; B29712; A34833; I46979
R;Freudenstein, J.; Wagner, S.; Luck, R.M.; Einspanier, R.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 171, 250-256, 1990
A;Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression i
A;Reference number: A35685; MUID:90365711; PMID:2393392
A;Accession: A35685
A;Molecule type: mRNA
A;Residues: 1-207 <FRE>
A;Cross-references: UNIPROT:P20414; UNIPARC:UPI0000136F8A; GB:M60073; NID:g163760; PIDN
A;Experimental source: ovary cDNA library
R;De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.
```

J. Biol. Chem. 264, 17445-17453, 1989
A;Title: Purification and characterization of two related but distinct metalloproteinase
A;Reference number: A34468; MUID:90008914; PMID:2551903
A;Accession: B34468
A;Molecule type: protein
A;Residues: 24-52,'X',54-57,'LY',60-61,'L',63-65,'L',67-68,'P' <DEC>
A;Cross-references: UNIPARC:UPI0000173239
A;Experimental source: culture medium of aortic endothelial cells
R;Kaczorek, M.; Honore, N.; Ribes, V.; Dehoux, P.; Cornet, P.; Cartwright, T.; Streeck,
Bio/Technology 5, 595-598, 1987
A;Title: Molecular cloning and synthesis of biologically active human tissue inhibitor c
A;Reference number: A29712
A;Accession: B29712
A;Molecule type: protein
A;Residues: 24-37 <KAC>
A;Cross-references: UNIPARC:UPI000017323A
A;Experimental source: culture medium of fibroblastic BC 21 cells
A;Note: protein inhibits angiogenesis
R;Moses, M.A.; Sudhalter, J.; Langer, R.
Science 248, 1408-1410, 1990
A;Title: Identification of an inhibitor of neovascularization from cartilage.
A;Reference number: A34833; MUID:90288433; PMID:1694043
A;Accession: A34833
A;Molecule type: protein
A;Residues: 24-51 <MOS>
A;Cross-references: UNIPARC:UPI000017323B
A;Experimental source: cartilage
R;Satoh, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.
Biol. Reprod. 50, 835-844, 1994
A;Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and ovidu
A;Reference number: I46979; MUID:94257757; PMID:8199264
A;Accession: I46979
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-207 <SAT>
A;Cross-references: UNIPARC:UPI0000136F8A; GB:S70841; NID:g546973; PIDN:AAB30892.1; PID:
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix met
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
A;Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F;24-93,26-122,36-147,150-197,155-160,168-189/Disulfide bonds: #status predicted
F;53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.5%; Score 995; DB 1; Length 207;
Best Local Similarity 87.0%; Pred. No. 5e-89;
Matches 180; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||| |:|||||||||| ||||||||||||||||||||:||||||||| |||:| ||||
Db          1 MAPFAPMASGILLLLWLTAPSRACTCVPPHPQTAFCNSDVVIRAKFVGTAEVNETALYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||:||| || || ||||:|||||||||||||| ||||||||||:| :| ||||
Db         61 YEIKMTKMFKGFSALRDAPDIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQLSNGHLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||:| |||||||||| |||||||||| |||||||| |||||||||| ||:|
Db        121 TCSFVAPWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||:|:|
Db        181 GFQSRHLACLPREPGLCTWQSLRAQMA 207
```

RESULT 4
I47061
collagenase inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: I47061
R;Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.
Mol. Cell. Endocrinol. 83, 65-71, 1992
A;Title: Differential screening of ovarian cDNA libraries detected the expression of t
A;Reference number: I47061; MUID:92201478; PMID:1312961
A;Accession: I47061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-207 <TAN>
A;Cross-references: UNIPROT:P35624; UNIPARC:UPI000016C64A; GB:S96211; NID:g247729; PID
C;Superfamily: metalloproteinase inhibitor

Query Match 86.4%; Score 971; DB 2; Length 207;
Best Local Similarity 84.1%; Pred. No. 1.1e-86;
Matches 174; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |:|| |||||||||||| ||||||||||||||||||:|||||||||| || |||  |||
Db          1 MSPFAPLASGILLLLWLTAPSRACTCVPPHPQTAFCSSDLVIRAKFVGAPEFNQTASYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||:||| ||||| ||||:|||||||||||||| |||:|||||:| :| ||||
Db         61 YEIKMTKMFKGFNALGDAPDIRFIYTPAMESVCGYFHRSQNRSQEFLIAGQLWNGHLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              |||||||||||| |||:|||: |  |||||||||| |||||||| |||||||||| ||:|
Db        121 TCSFVAPWNSLSSAQRQGFTEIYAAGCEECTVFPCTSIPCKLQSDTHCLWTDQLLTGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||:|||||:||||||| ::|
Db        181 GFQSRHLACMPREPGMCTWQSLRPRVA 207
```

RESULT 5
I46964
metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46964
R;Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.
Endocrinology 134, 344-352, 1994
A;Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases
eal tissue.
A;Reference number: I46964; MUID:94102210; PMID:8275949
A;Accession: I46964
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-207 <SMI>
A;Cross-references: UNIPROT:P50122; UNIPARC:UPI0000136F92; GB:S67450; NID:g456989; PII
C;Superfamily: metalloproteinase inhibitor

Query Match 85.5%; Score 961; DB 2; Length 207;
Best Local Similarity 85.7%; Pred. No. 9.8e-86;
Matches 174; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              || | |  ||||||||| |||||||||||||||||||::||||||||| |||:| ||||
Db          1 MALFAPTVSGILLLLWLTAPSRACTCVPPHPQTAFCNSEVVIRAKFVGTAEVNETALYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||:||| || || ||||:|||||||||||||| ||||||||||:| :| ||||
Db         61 YEIKMTKMFKGFSALRDAPDIRFIYTPAMESVCGYFHRSQNRSEEFLIAGQLSNGHLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||:| |||||||||| |||||||||| |||||||| ||||||||||:| ||:|
Db        121 TCSFVAPWNSMSSAQRRGFTKTYAAGCEECTVFPCSSIPCKLQSDTHCLWTDQLLTGSDK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLR 203
              |||||||||||||||:|||||||
Db        181 GFQSRHLACLPREPGMCTWQSLR 203
```

```
RESULT 6
A33350
metalloproteinase inhibitor 1 precursor - rabbit
N;Alternate names: TIMP-1; tissue inhibitor of metalloproteinases 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Jun-1992 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A33350; A30864
R;Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Notter, R.H.; Quible, D.J.
J. Biol. Chem. 264, 7092-7095, 1989
A;Title: Hyperoxic exposure alters gene expression in the lung. Induction of the tissue
A;Reference number: A33350; MUID:89214135; PMID:2708356
A;Accession: A33350
A;Molecule type: mRNA
A;Residues: 1-206 <HOR>
A;Cross-references: UNIPROT:P20614; UNIPARC:UPI0000136F90; GB:J04712; NID:g165742; PIDN:
A;Experimental source: hyperoxi-exposed lung of New Zealand White rabbits
C;Comment: Expression of this protein in the lung is induced 6-fold by hyperoxia.
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix met
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
A;Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-206/Product: metalloproteinase inhibitor 1 #status predicted <MAT>
F;24-93,26-122,36-147,150-196,155-160,168-188/Disulfide bonds: #status predicted
F;53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             80.3%;  Score 902.5;  DB 1;  Length 206;
  Best Local Similarity   80.8%;  Pred. No. 4.6e-80;
  Matches  164;  Conservative   13;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              |||   ||| :||||||:|||||||||||||||||||||||||||||| |||| ||||||
Db          1 MAPLAALASSMLLLLWLVAPSRACTCVPPHPQTAFCNSDLVIRAKFVGAPEVNHTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |||| |||:||| ||| | |||||||||||||||| |:| ||||||||||:|::||||||
Db         61 YEIKTTKMFKGFDALGHATDIRFVYTPAMESVCGYSHKSQNRSEEFLIAGQLRNGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||| |||||| :|| |||||| ||: |||| | |||| |:| ||||||| | ||:|
Db        121 TCSFVVPWNSLSFSQRSGFTKTYAAGCDMCTVFACASIPCHLESDTHCLWTDSSL-GSDK 179

Qy        181 GFQSRHLACLPREPGLCTWQSLR 203
              |||||||||||:||||| |:|||
Db        180 GFQSRHLACLPQEPGLCAWESLR 202


RESULT 7
A26106
metalloproteinase inhibitor 1 precursor - mouse
N;Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibit
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1988 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A26917; A26106; A26633; A05276
R;Johnson, M.D.; Housey, G.M.; Kirschmeier, P.T.; Weinstein, I.B.
Mol. Cell. Biol. 7, 2821-2829, 1987
A;Title: Molecular cloning of gene sequences regulated by tumor promoters and mitogens t
A;Reference number: A26917; MUID:88038821; PMID:3670294
A;Accession: A26917
A;Molecule type: mRNA
A;Residues: 1-205 <JOH>
A;Cross-references: UNIPROT:P12032; UNIPARC:UPI00000018BB; GB:M17243; NID:g202111; PIDN:
A;Experimental source: embryonic fibroblast cDNA library
R;Edwards, D.R.; Waterhouse, P.; Holman, M.L.; Denhardt, D.T.
Nucleic Acids Res. 14, 8863-8878, 1986
A;Title: A growth-responsive gene (16C8) in normal mouse fibroblasts homologous to a hum
pts.
A;Reference number: A26106; MUID:87066763; PMID:3024122
A;Accession: A26106
A;Molecule type: mRNA
A;Residues: 1-205 <EDW>
A;Cross-references: UNIPARC:UPI00000018BB; GB:X04684; NID:g49702; PIDN:CAA28387.1; PID
A;Experimental source: embryonic fibroblast cDNA library
R;Gewert, D.R.; Coulombe, B.; Castelino, M.; Skup, D.; Williams, B.R.G.
EMBO J. 6, 651-657, 1987
A;Title: Characterization and expression of a murine gene homologous to human EPA/TIMP
A;Reference number: A26633; MUID:87218524; PMID:3034603
A;Accession: A26633
A;Molecule type: DNA
A;Residues: 1-51,'R',53-66,'M',67-116,'KF',119-120,'N',122-138,'V',140-142,'KN',144-193
A;Cross-references: UNIPARC:UPI000016394C; GB:M28312; NID:g193040; PIDN:AAB42179.1; PID
R;Skup, D.; Windass, J.D.; Sor, F.; George, H.; Williams, B.R.G.; Fukuhara, H.; De Maey
Nucleic Acids Res. 10, 3069-3084, 1982
A;Title: Molecular cloning of partial cDNA copies of two distinct mouse IFN-beta mRNAs
A;Reference number: A93424; MUID:82247191; PMID:6179042
A;Accession: A05276
A;Molecule type: mRNA
A;Residues: 168-193,'L',195-205 <SKU>
A;Cross-references: UNIPARC:UPI00000E8041; GB:V00755; GB:J00425; NID:g51554; PIDN:CAA24
A;Note: authors thought this clone represented a form of interferon beta
C;Genetics:
A;Gene: Timp
A;Map position: X
A;Introns: 41/3; 68/3; 110/3; 152/3
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix me
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiatin
A;Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agen
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patt
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhib
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-205/Product: metalloproteinase inhibitor 1 #status predicted <MAT>
F;25-94,27-123,37-148,151-197,156-161,169-189/Disulfide bonds: #status predicted
F;54,102/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             74.5%;  Score 837.5;  DB 1;  Length 205;
  Best Local Similarity   74.3%;  Pred. No. 9.2e-74;
  Matches  150;  Conservative   26;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||  |||||||||| ||| |:||:| ||||||||||||||||||:|:||:|:||||||
Db          2 MAPFASLASGILLLLSLIASSKACSCAPPHPQTAFCNSDLVIRAKFMGSPEINETTLYQR 61

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |:|||||| |||:|:|:|||||: ||| |||:||| |:| |||||||| |:|::| |||:
Db         62 YKIKMTKMLKGFKAVGNAADIRYAYTPVMESLCGYAHKSQNRSEEFLITGRLRNGNLHIS 121

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              |||: || :|| ||:| |:|||: ||  |||||||||||||:| |||||||:| |||
Db        122 ACSFLVPWRTLSPAQQRAFSKTYSAGCGVCTVFPCLSIPCKLESDTHCLWTDQVLVGSE- 180

Qy        181 GFQSRHLACLPREPGLCTWQSL 202
              :|||| ||||| ||||||:||
Db        181 DYQSRHFACLPRNPGLCTWRSL 202


RESULT 8
JC2557
metalloproteinase inhibitor 1 precursor - rat
N;Alternate names: TIMP-1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC2557; B39120; S20326
R;Okada, A.; Garnier, J.M.; Vicaire, S.; Basset, P.
Gene 147, 301-302, 1994
A;Title: Cloning of the cDNA encoding rat tissue inhibitor of metalloproteinase 1 (TIMP-
A;Reference number: JC2557; MUID:95011636; PMID:7926820
A;Accession: JC2557
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-217 <OKA>
A;Cross-references: UNIPROT:P30120; UNIPARC:UPI0000136F91; EMBL:U06179; NID:g468057; PID
```

R;Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, M.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991
A;Title: Angiotensin II induces secretion of plasminogen activator inhibitor 1 and a tis
A;Reference number: A39120; MUID:91156719; PMID:2000398
A;Accession: B39120
A;Status: preliminary
A;Molecule type: protein
A;Residues: 24-36,'B',38,'B',40-42,'X',44 <OLS>
A;Cross-references: UNIPARC:UPI000017323C
R;Roswit, W.T.; McCourt, D.W.; Partridge, N.C.; Jeffrey, J.J.
Arch. Biochem. Biophys. 292, 402-410, 1992
A;Title: Purification and sequence analysis of two rat tissue inhibitors of metalloprote
A;Reference number: S20325; MUID:92117648; PMID:1309971
A;Accession: S20326
A;Molecule type: protein
A;Residues: 24-45 <ROS>
A;Cross-references: UNIPARC:UPI000017323D
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix met
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
A;Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-217/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F;101,130/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.8%; Score 818; DB 1; Length 217;
Best Local Similarity 72.3%; Pred. No. 7.7e-72;
Matches 146; Conservative 24; Mismatches 32; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||  |||||||||| ||| |:||:| | |||||||||||||||||:|:||: :||||||
Db          1 MAPFASLASGILLLLSLIASSKACSCAPTHPQTAFCNSDLVIRAKFMGSPEIIETTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              |||||||| ||| |:|:|   || |||||||:||| |:| ||||||||||:|::| ||||
Db         61 YEIKMTKMLKGFDAVGNATGFRFAYTPAMESLCGYVHKSQNRSEEFLIAGRLRNGNLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
               |||: ||::|| ||:: | |||: ||  |||||| :|||||:| :|||||||:| ||||
Db        121 ACSFLVPWHNLSPAQQKAFVKTYSAGCGVCTVFPCSAIPCKLESDSHCLWTDQILMGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSL 202
              |:|| | ||||| | ||||| |
Db        181 GYQSDHFACLPRNPDLCTWQYL 202
```

RESULT 9
JH0683
metalloproteinase inhibitor 2 precursor - mouse
N;Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0683; JC1234; S18428; S15987; S26189
R;Shimizu, S.; Malik, K.; Sejima, H.; Kishi, J.; Hayakawa, T.; Koiwai, O.
Gene 114, 291-292, 1992
A;Title: Cloning and sequencing of the cDNA encoding a mouse tissue inhibitor of metallo
A;Reference number: JH0683; MUID:92290292; PMID:1601312
A;Accession: JH0683
A;Molecule type: mRNA
A;Residues: 1-220 <SHI>
A;Cross-references: UNIPROT:P25785; UNIPARC:UPI00000278E8; EMBL:X62622; NID:g54801; PIDN
A;Experimental source: 3T3 fibroblast, strain Balb/c
R;Leco, K.J.; Hayden, L.J.; Sharma, R.R.; Rocheleau, H.; Greenberg, A.H.; Edwards, D.R.
Gene 117, 209-217, 1992
A;Title: Differential regulation of TIMP-1 and TIMP-2 mRNA expression in normal and Ha-r
A;Reference number: JC1234; MUID:92347695; PMID:1639268
A;Accession: JC1234
A;Molecule type: mRNA
A;Residues: 1-11,'H',13-20,'L',22-194,'E',196-220 <LEC>
A;Cross-references: UNIPARC:UPI000016D07D; GB:M93954; NID:g202053; PIDN:AAA40446.1; PID:

R;Kishi, J.
Matrix 11, 373, 1991
A;Title: Correction.
A;Reference number: S18428; MUID:92244125; PMID:1667327
A;Accession: S18428
A;Molecule type: protein
A;Residues: 27-46,'H',48,50-53,'VD',56,'DY' <KIS>
A;Cross-references: UNIPARC:UPI0000173246
R;Kishi, J.I.; Ogawa, K.; Yamamoto, S.; Hayakawa, T.
Matrix 11, 10-16, 1991
A;Title: Purification and characterization of a new tissue inhibitor of metalloprotein
A;Reference number: S15987; MUID:91226375; PMID:1851244
A;Accession: S15987
A;Molecule type: protein
A;Residues: 27-46,'HLX',50-52,'LX',55-56,'DXX',60,'X',62 <KI2>
A;Cross-references: UNIPARC:UPI0000173247
A;Note: this sequence has been revised in reference S18428
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix m
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiati
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>
F;27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 37.4%; Score 420.5; DB 1; Length 220;
Best Local Similarity 42.8%; Pred. No. 2.8e-33;
Matches 86; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

```
Qy          7 LASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQ-TTLYQ------ 59
              || |:||| |: |: ||:| | ||| ||||:|:||||| |   ||:    :|
Db         10 LALGLLLLASLVRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRI 69

Qy         60 RYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLLH 118
              :|||| ||:|     |   || |:||    :|||         :|:||||| : || :|
Db         70 QYEIKQIKMFK-----GPDKDIEFIYTAPSSAVCG-VSLDVGGKKEYLIAGKAEGDGKMH 123

Qy        119 ITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGS 178
              || | |: ||::||: |::     | :|| || :  |  ||| : |   ||| | : : |
Db        124 ITLCDFIVPWDTLSITQKKSLNHRYQMGC-ECKITRCPMIPCYISSPDECLWMDWVTEKS 182

Qy        179 EKGFQSRHLACLPREPGLCTW 199
               | |::  ||: |  | | |
Db        183 INGHQAKFFACIKRSDGSCAW 203
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RESULT 10
I53415
tissue inhibitor of metalloproteinase type 2 - rat
C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: I53415
R;Santoro, M.; Battaglia, C.; Zhang, L.; Carlomagno, F.; Martelli, M.L.; Salvatore, D
Exp. Cell Res. 213, 398-403, 1994
A;Title: Cloning of the rat tissue inhibitor of metalloproteinases type 2 (TIMP-2) ge
A;Reference number: I53415; MUID:94326839; PMID:8050496
A;Accession: I53415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-220 <RES>
A;Cross-references: UNIPARC:UPI000000102A; GB:S72594; NID:g619232; PIDN:AAC60687.1; P
C;Genetics:
A;Gene: TIMP-2
C;Superfamily: metalloproteinase inhibitor

Query Match 37.4%; Score 420.5; DB 2; Length 220;
Best Local Similarity 42.8%; Pred. No. 2.8e-33;
Matches 86; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

```
Qy          7 LASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQ-TTLYQ------ 59
              || |:||| |: |: ||:| | ||| ||||:|:||||| |   ||:    :|
Db         10 LALGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRI 69
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Qy          60 RYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLLH 118
               :|||| ||:|     |   || |:||    :|||         :|:||||| : || :|
Db          70 QYEIKQIKMFK-----GPDKDIEFIYTAPSSAVCG-VSLDVGGKKEYLIAGKAEGDGKMH 123

Qy         119 ITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGS 178
               || | |: ||::||: |::     | :|| || :  |  ||| : |   ||| | : : |
Db         124 ITLCDFIVPWDTLSITQKKSLNHRYQMGC-ECKITRCPMIPCYISSPDECLWMDWVTEKS 182

Qy         179 EKGFQSRHLACLPREPGLCTW 199
                 | |::  ||: |  | | |
Db         183 INGHQAKFFACIKRSDGSCAW 203
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RESULT 11
S45683
metalloproteinase inhibitor 2 precursor - rat
N;Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S45683; S20325; S60160
R;Cook, T.F.; Burke, J.S.; Bergman, K.D.; Quinn, C.O.; Jeffrey, J.J.; Partridge, N.C.
Arch. Biochem. Biophys. 311, 313-320, 1994
A;Title: Cloning and regulation of rat tissue inhibitor of metalloproteinases-2 in osteo
A;Reference number: S45683; MUID:94263207; PMID:8203893
A;Accession: S45683
A;Molecule type: mRNA
A;Residues: 1-220 <COO>
A;Cross-references: UNIPROT:P30121; UNIPARC:UPI00001707D2; GB:U14526; NID:g540204; PIDN:
R;Roswit, W.T.; McCourt, D.W.; Partridge, N.C.; Jeffrey, J.J.
Arch. Biochem. Biophys. 292, 402-410, 1992
A;Title: Purification and sequence analysis of two rat tissue inhibitors of metalloprote
A;Reference number: S20325; MUID:92117648; PMID:1309971
A;Accession: S20325
A;Molecule type: protein
A;Residues: 27-48 <ROS>
A;Cross-references: UNIPARC:UPI0000173248
R;Gibbons, K.L.; O'Grady, R.L.; Piper, A.A.
submitted to the EMBL Data Library, June 1995
A;Description: Rat tissue inhibitor of metalloproteinases-2: cDNA cloning and sequence a
A;Reference number: S60160
A;Accession: S60160
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-6,'S',8-20,'V',22-152,'E',154-220 <GIB>
A;Cross-references: UNIPARC:UPI0000173249; EMBL:L31884
C;Genetics:
A;Gene: TIMP-2
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix met
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
F;27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

  Query Match   37.1%; Score 417.5; DB 1; Length 220;
  Best Local Similarity 42.3%; Pred. No. 5.4e-33;
  Matches   85; Conservative   31; Mismatches   70; Indels   15; Gaps   6;

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Qy           7 LASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQ-TTLYQ------ 59
               || |:||| |: |: ||:| | ||| ||||:|:||||| |   ||:    :|
Db          10 LALGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRI 69

Qy          60 RYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLLH 118
               :|||| ||:|     |   || |:||    :|||         :|:||||| : || :|
Db          70 QYEIKQIKMFK-----GPDKDIEFIYTAPSSAVCG-VSLDVGGKKEYLIAGKAEGDGKMH 123

Qy         119 ITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGS 178
               || | |: ||::||: |::     | :|| :| :  |  ||| : |   ||| | : : |
Db         124 ITLCDFIVPWDTLSITQKKSLNHRYQMGC-QCKITRCPMIPCYISSPDECLWMDWVTEKS 182

Qy         179 EKGFQSRHLACLPREPGLCTW 199
                 | |::  ||: |  | | |
Db         183 INGHQAKFFACIKRSDGSCAW 203
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RESULT 12
A37128
metalloproteinase inhibitor 2 precursor [validated] - human
N;Alternate names: chondrocyte-derived angiogenesis inhibitor; TIMP-2; tissue inhibitor
C;Species: Homo sapiens (man)
C;Date: 08-Mar-1991 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A37128; B35996; A34464; A34415; S21303; S20319; S17165; S58794
R;Stetler-Stevenson, W.G.; Brown, P.D.; Onisto, M.; Levy, A.T.; Liotta, L.A.
J. Biol. Chem. 265, 13933-13938, 1990
A;Title: Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA expression in tumor cel
A;Reference number: A37128; MUID:90338014; PMID:2380196
A;Accession: A37128
A;Molecule type: mRNA
A;Residues: 1-220 <STE>
A;Cross-references: UNIPROT:P16035; UNIPARC:UPI0000136F99; GB:J05593; NID:g339706; PIDN
A;Experimental source: A2058 melanoma cell cDNA library
R;Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, 1990
A;Title: cDNA cloning and expression of a metalloproteinase inhibitor related to tissue
A;Reference number: A35996; MUID:90207285; PMID:2157214
A;Accession: B35996
A;Molecule type: mRNA
A;Residues: 1-220 <BOO>
A;Cross-references: UNIPARC:UPI0000136F99; GB:M32304; NID:g187522; PIDN:AAA59581.1; PID
A;Experimental source: fetal aorta cDNA library
R;Stetler-Stevenson, W.G.; Krutzsch, H.C.; Liotta, L.A.
J. Biol. Chem. 264, 17374-17378, 1989
A;Title: Tissue inhibitor of metalloproteinase (TIMP-2). A new member of the metallopro
A;Reference number: A34464; MUID:90008902; PMID:2793861
A;Accession: A34464
A;Molecule type: protein
A;Residues: 27-77,'K',79-81,'I',83-100,'E',102-117;119-121,'R',123-149,'Q',151-174,'T',1
A;Cross-references: UNIPARC:UPI000017323E; UNIPARC:UPI000017323F
A;Experimental source: serum-free culture medium of A2058 cells
R;Goldberg, G.I.; Marmer, B.L.; Grant, G.A.; Eisen, A.Z.; Wilhelm, S.; He, C.
Proc. Natl. Acad. Sci. U.S.A. 86, 8207-8211, 1989
A;Title: Human 72-kilodalton type IV collagenase forms a complex with a tissue inhibitor
A;Reference number: A34415; MUID:90046765; PMID:2554304
A;Accession: A34415
A;Molecule type: protein
A;Residues: 30-51;124-141;159-173 <GOL>
A;Cross-references: UNIPARC:UPI0000173240; UNIPARC:UPI0000173241; UNIPARC:UPI0000173242
R;Malik, K.; Sejima, H.; Aoki, T.; Iwata, K.
submitted to the EMBL Data Library, August 1990
A;Description: Nucleotide sequence of a TIMP-II cDNA.
A;Reference number: S21303
A;Accession: S21303
A;Molecule type: mRNA
A;Residues: 30-95,'V',97-214 <MAL>
A;Cross-references: UNIPARC:UPI000016B0E4; EMBL:X54533; NID:g37180; PIDN:CAA38400.1; PID
R;Osthues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.
FEBS Lett. 296, 16-20, 1992
A;Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP
A;Reference number: S20318; MUID:92111776; PMID:1730286
A;Accession: S20319
A;Molecule type: protein
A;Residues: 'X',28,'X',30-38,'X',40-41 <OST>
A;Cross-references: UNIPARC:UPI0000173243
A;Experimental source: rheumatoid synovial fluid
R;Ward, R.V.; Hembry, R.M.; Reynolds, J.J.; Murphy, G.
Biochem. J. 278, 179-187, 1991
A;Title: The purification of tissue inhibitor of metalloproteinases-2 from its 72 kDa pr
A;Reference number: S17165; MUID:91354200; PMID:1909113
A;Accession: S17165
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27,'X',29,'X',31-38 <WAR>
A;Cross-references: UNIPARC:UPI0000173244

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R;Ohba, Y.; Goto, Y.; Kimura, Y.; Suzuki, F.; Hisa, T.; Takahashi, K.; Takigawa, M.
Biochim. Biophys. Acta 1245, 1-8, 1995
A;Title: Purification of an angiogenesis inhibitor from culture medium conditioned by a
A;Reference number: S58794; MUID:95383380; PMID:7544625
A;Accession: S58794
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-37 <OHB>
A;Cross-references: UNIPARC:UPI0000173245
C;Genetics:
A;Gene: GDB:TIMP2
A;Cross-references: GDB:132612; OMIM:188825
A;Map position: 17q25-17q25
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix met
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>
F;27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

  Query Match             37.0%;  Score 415.5;  DB 1;  Length 220;
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  Matches   85;  Conservative   30;  Mismatches   71;  Indels   15;  Gaps    6;

Qy          7 LASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQ-TTLYQ------ 59
              || |:|||  |: |: ||:| | ||| ||||:|:||||| |   ||:    :|
Db         10 LALGLLLLATLLRPADACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRI 69

Qy         60 RYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLLH 118
              :|||| ||:|     |   || |:||    :|||         :|:||||| : || :|
Db         70 QYEIKQIKMFK-----GPEKDIEFIYTAPSSAVCG-VSLDVGGKKEYLIAGKAEGDGKMH 123

Qy        119 ITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGS 178
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Db        124 ITLCDFIVPWDTLSTTQKKSLNHRYQMGC-ECKITRCPMIPCYISSPDECLWMDWVTEKN 182

Qy        179 EKGFQSRHLACLPREPGLCTW 199
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Db        183 INGHQAKFFACIKRSDGSCAW 203


RESULT 13
A35996
metalloproteinase inhibitor 2 precursor - bovine
N;Alternate names: collagenase inhibitor; tissue inhibitor of metalloproteinases (TIMP-2
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Nov-1990 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A35996; A34468; A25322; S28151
R;Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, 1990
A;Title: cDNA cloning and expression of a metalloproteinase inhibitor related to tissue
A;Reference number: A35996; MUID:90207285; PMID:2157214
A;Accession: A35996
A;Molecule type: mRNA
A;Residues: 1-220 <BOO>
A;Cross-references: UNIPROT:P16368; UNIPARC:UPI0000136F93; GB:M32303; NID:g163341; PIDN:
A;Experimental source: aortic endothelial cDNA library
R;De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.
J. Biol. Chem. 264, 17445-17453, 1989
A;Title: Purification and characterization of two related but distinct metalloproteinase
A;Reference number: A34468; MUID:90008914; PMID:2551903
A;Accession: A34468
A;Molecule type: protein
A;Residues: 27-71 <DEC>
A;Cross-references: UNIPARC:UPI000017324A
A;Experimental source: culture medium of aortic endothelial cells
R;Murray, J.B.; Allison, K.; Sudhalter, J.; Langer, R.
J. Biol. Chem. 261, 4154-4159, 1986
A;Title: Purification and partial amino acid sequence of a bovine cartilage-derived coll
A;Reference number: A25322; MUID:86140235; PMID:3005321
A;Accession: A25322
A;Molecule type: protein
A;Residues: 27-41,'C',43-55,'EX',58-59,'X',61-66,'XS',69-71 <MUR>
A;Cross-references: UNIPARC:UPI000017324B
A;Experimental source: cartilage
R;DeClerck, Y.A.; Yean, T.D.; Lee, Y.; Tomich, J.M.; Langley, K.E.
Biochem. J. 289, 65-69, 1993
A;Title: Characterization of the functional domain of tissue inhibitor of metalloprotei
A;Reference number: S28151; MUID:93143691; PMID:8424773
A;Contents: annotation; functional domain
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix me
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiatir
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
F;27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

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Qy          6 PLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQ-TTLYQ----- 59
              |||  :|||  |:  : ||:| | ||| ||||:|:||||| |   ||:    :|
Db          9 PLAFCLLLLGTLLPRADACSCSPVHPQQAFCNADIVIRAKAVNKKEVDSGNDIYGNPIKR 68

Qy         60 -RYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLL 117
               :|||| ||:|     |   || |:||    :|||         :|:||||| : :| :
Db         69 IQYEIKQIKMFK-----GPDQDIEFIYTAPAAAVCG-VSLDIGGKKEYLIAGKAEGNGNM 122

Qy        118 HITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQG 177
              ||| | |: ||::||  |::     | :|| || :  |  ||| : |    ||| | : :
Db        123 HITLCDFIVPWDTLSATQKKSLNHRYQMGC-ECKITRCPMIPCYISSPDECLWMDWVTEK 181

Qy        178 SEKGFQSRHLACLPREPGLCTW 199
              :  | |::  ||: |  | | |
Db        182 NINGHQAKFFACIKRSDGSCAW 203


RESULT 14
S45317
metalloproteinase inhibitor 3 precursor [validated] - human
N;Alternate names: mig-5 protein; TIMP-3; tissue inhibitor of metalloproteinases 3
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S45317; S59515; S53870; I38023; A49614; C56937; I53025; S47041
R;Uria, J.A.; Ferrando, A.A.; Velasco, G.; Freije, J.M.P.; Lopez-Otin, C.
Cancer Res. 54, 2091-2094, 1994
A;Title: Structure and expression in breast tumors of human TIMP-3, a new member of the
A;Reference number: S45317; MUID:94228524; PMID:8174111
A;Accession: S45317
A;Molecule type: mRNA
A;Residues: 1-211 <URI>
A;Cross-references: UNIPROT:P35625; UNIPARC:UPI000005F30A; EMBL:X76227; NID:g495251; PI
A;Experimental source: breast tumor cDNA library
R;Silbiger, S.M.; Jacobsen, V.L.; Cupples, R.L.; Koski, R.A.
Gene 141, 293-297, 1994
A;Title: Cloning of cDNAs encoding human TIMP-3, a novel member of the tissue inhibitor
A;Reference number: S59515; MUID:94215920; PMID:8163205
A;Accession: S59515
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <SIL>
A;Cross-references: UNIPARC:UPI000005F30A; EMBL:U02571; NID:g472309; PIDN:AAA17672.1; P
R;Kishnani, N.S.; Staskus, P.W.; Yang, T.T.; Masiarz, F.R.; Hawkes, S.P.
Matrix Biol. 14, 479-488, 1994
A;Title: Identification and characterization of human tissue inhibitor of metalloprotei
A;Reference number: S53870
A;Accession: S53870
A;Molecule type: protein
A;Residues: 'X',25,'XX',28,'X',30-35,'X',37,'X',39-41 <KIS>
A;Cross-references: UNIPARC:UPI000017324C
R;Wick, M.; Buerger, C.; Brueselbach, S.; Lucibello, F.C.; Mueller, R.
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J. Biol. Chem. 269, 18953-18960, 1994
A;Title: A novel member of human tissue inhibitor of metalloproteinases (TIMP) gene fami
A;Reference number: I38023; MUID:94308155; PMID:8034652
A;Accession: I38023
A;Molecule type: mRNA
A;Residues: 1-15,'W',17,'T',20-21,'PR',24-201,'X',203-211 <RES>
A;Cross-references: UNIPARC:UPI000016AD5E; EMBL:Z30183; NID:g520931; PIDN:CAA82918.1; PI
A;Experimental source: fibroblast cell line WI-38
R;Apte, S.S.; Mattei, M.G.; Olsen, B.R.
Genomics 19, 86-90, 1994
A;Title: Cloning of the cDNA encoding human tissue inhibitor of metalloproteinases-3 (TI
A;Reference number: A49614; MUID:94245184; PMID:8188246
A;Accession: A49614
A;Molecule type: mRNA
A;Residues: 14-20,'R',23-211 <APT>
A;Cross-references: UNIPARC:UPI000016B0E5; GB:L15078; NID:g407034; PIDN:AAA21815.1; PID:
A;Experimental source: placenta cDNA library
R;Apte, S.S.; Olsen, B.R.; Murphy, G.
J. Biol. Chem. 270, 14313-14318, 1995
A;Title: The gene structure of tissue inhibitor of metalloproteinases (TIMP)-3 and its i
A;Reference number: A56937; MUID:95301511; PMID:7782289
A;Accession: C56937
A;Molecule type: protein
A;Residues: 'X',25,'X',27-35,'X',37 <AP2>
A;Cross-references: UNIPARC:UPI000017324D
R;Wilde, C.G.; Hawkins, P.R.; Coleman, R.T.; Levine, W.B.; Delegeane, A.M.; Okamoto, P.M
DNA Cell Biol. 13, 711-718, 1994
A;Title: Cloning and characterization of human tissue inhibitor of metalloproteinases-3.
A;Reference number: I53025; MUID:95290091; PMID:7772252
A;Accession: I53025
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-211 <RE2>
A;Cross-references: UNIPARC:UPI000005F30A; GB:S78453; NID:g998825; PIDN:AAB34532.1; PID:
C;Genetics:
A;Gene: GDB:TIMP3
A;Cross-references: GDB:138175; OMIM:188826
A;Map position: 22q12.1-22q13.2
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix met
A;Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
C;Superfamily: metalloproteinase inhibitor
C;Keywords: extracellular matrix; metalloproteinase inhibitor
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-211/Product: metalloproteinase inhibitor 3 #status experimental <MAT>
F;24-91,26-118,36-143,145-192,150-155,163-184/Disulfide bonds: #status predicted

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Matches 78; Conservative 38; Mismatches 66; Indels 15; Gaps 7;

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               |:::||  | :    : |||| | ||| ||||||:||||| ||   | :    ||   |
Db           6 GLIVLLGSWSLGDWGAEACTCSPSHPQDAFCNSDIVIRAKVVGKKLVKEGPFGTLV--YT 63

Qy          63 IKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTC 122
               ||  |||:||  :     :::::| | ||:||   :      ::|: |:: || ::   |
Db          64 IKQMKMYRGFTKM---PHVQYIHTEASESLCGL--KLEVNKYQYLLTGRVYDGKMYTGLC 118

Qy         123 SFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGF 182
               :||  |: |:|:||:|    | :||  | :  |  :|| : |   |||||  |       |:
Db         119 NFVERWDQLTLSQRKGLNYRYHLGC-NCKIKSCYYLPCFVTSKNECLWTDMLSNFGYPGY 177

Qy         183 QSRHLACLPREPGLCTW 199
               ||:| ||: :: | |:|
Db         178 QSKHYACIRQKGGYCSW 194
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RESULT 15
S38624
metalloproteinase inhibitor 2 precursor - long-tailed hamster (fragment)
N;Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 06-Jan-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S38624
R;Suzuki, Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38624
A;Accession: S38624
A;Molecule type: mRNA
A;Residues: 1-196 <SUZ>
A;Cross-references: UNIPROT:Q60453; UNIPARC:UPI0000136F97; EMBL:X75924; NID:g414876; PID
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix met
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C;Superfamily: metalloproteinase inhibitor
C;Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F;3-196/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
F;3-74,5-103,15-128,130-177,135-140,148-169/Disulfide bonds: #status predicted

Query Match 34.6%; Score 388.5; DB 1; Length 196;
Best Local Similarity 42.5%; Pred. No. 3.1e-30;
Matches 79; Conservative 26; Mismatches 66; Indels 15; Gaps 6;

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               |||:| | ||| ||||:|:||||| |    ||:    :|       :||||  ||:|
Db           1 RACSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFK---- 56

Qy          75 LGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQ-DGLLHITTCSFVAPWNSLSL 133
                |   || |:||    :|||          :|:||||| : || :||| | |: ||::||
Db          57 -GPDKDIEFIYTAPSSAVCG-VSLDVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLST 114

Qy         134 AQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPRE 193
                |::     | :|| || :  |  ||| : |   ||| | : : |  | |::  ||: |
Db         115 TQKKSLNHRYQMGC-ECKITRCPMIPCYISSPDECLWMDWVTEKSINGHQAKFFACIKRS 173

Qy         194 PGLCTW 199
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Db         174 DGSCAW 179
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:05 ; Search time 79.703 Seconds
(without alignments)
1141.129 Million cell updates/sec

Title: US-10-734-564-100
Perfect score: 1124
Sequence: 1 MAPFEPLASGILLLLWLIAP.....ACLPREPGLCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1124	100.0	207	1	AAP60592	Aap60592 Sequence
2	1124	100.0	207	1	AAP60275	Aap60275 Sequence
3	1124	100.0	207	1	AAP60786	Aap60786 Sequence
4	1124	100.0	207	2	AAW30309	Aaw30309 Human TIM
5	1124	100.0	207	2	AAY08933	Aay08933 Human TIM
6	1124	100.0	207	3	AAB19073	Aab19073 Inhibitor
7	1124	100.0	207	7	ADC37139	Adc37139 Human tis
8	1124	100.0	207	7	ADL78829	Adl78829 Human tis
9	1124	100.0	207	8	ADG25251	Adg25251 Human TIM
10	1124	100.0	207	8	ADQ07367	Adq07367 Human tis
11	1124	100.0	207	8	ADP75947	Adp75947 Human TIM
12	1124	100.0	207	8	ADQ29674	Adq29674 Human col
13	1124	100.0	207	8	ADP23249	Adp23249 PRO polyp
14	1124	100.0	207	8	ADU06696	Adu06696 Novel bro
15	1124	100.0	207	9	ADV70205	Adv70205 Tumor-ass
16	1124	100.0	207	9	ADY14618	Ady14618 PRO polyp
17	1124	100.0	207	9	AEB87782	Aeb87782 Human TIM
18	1121	99.7	207	1	AAP60593	Aap60593 Sequence
19	1120	99.6	207	4	AAG89171	Aag89171 Human sec
20	1119	99.6	207	4	AAM93377	Aam93377 Human pol
21	1119	99.6	207	8	ADL30920	Adl30920 Human pro
22	1118	99.5	207	9	ADZ70216	Adz70216 Human tis
23	1104	98.2	207	2	AAR65005	Aar65005 Human tis
24	1073.5	95.5	203	8	ADO28641	Ado28641 Human TIM
25	1034	92.0	204	5	ABP42206	Abp42206 Human ova
26	1010	89.9	580	5	AAU99889	Aau99889 rTAP1 fus
27	1009	89.8	184	5	AAU99875	Aau99875 Human tis
28	1009	89.8	184	8	ADG14621	Adg14621 Human TIM
29	1009	89.8	580	5	AAU99882	Aau99882 TAP1 fusi
30	995	88.5	207	2	AAR65003	Aar65003 Cattle ti
31	951	84.6	207	2	AAR65004	Aar65004 Pig tissu
32	895	79.6	166	8	ADR87602	Adr87602 Human TIM
33	892.5	79.4	206	2	AAR65006	Aar65006 Rabbit ti
34	827.5	73.6	205	2	AAR65007	Aar65007 Mouse tis
35	818	72.8	217	7	ADD45970	Add45970 Rat Prote
36	782.5	69.6	183	3	AAB44149	Aab44149 Human can
37	779.5	69.4	207	2	AAR65008	Aar65008 Mouse tis
38	728.5	64.8	212	5	ABP42381	Abp42381 Human ova
39	715	63.6	162	5	ABP42434	Abp42434 Human ova
40	691	61.5	128	5	AAU99887	Aau99887 Human TIM
41	683	60.8	522	5	AAU99885	Aau99885 rN-TAP1 f
42	682	60.7	127	5	AAU99886	Aau99886 Human TIM
43	682	60.7	522	5	AAU99883	Aau99883 NTAP1 fus
44	587.5	52.3	136	8	ADO07052	Ado07052 Human pro
45	543	48.3	156	8	ADP45514	Adp45514 Human col

ALIGNMENTS

RESULT 1
AAP60592
ID AAP60592 standard; protein; 207 AA.
XX
AC AAP60592;
XX
DT 13-AUG-1991 (first entry)
XX
DE Sequence of a human protein having erythroid potentiating activity (EPA).
XX
KW Erythroid precursor growth; anaemia therapy.
XX
OS Homo sapiens.
XX
PN WO8602100-A.
XX
PD 10-APR-1986.
XX
PF 01-OCT-1984; 84US-00656590.
XX
PR 01-OCT-1984; 84US-00656590.
XX
PA (SANO) SANDOZ LTD.
PA (REGC) REGENTS OF UNIV OF CALIFO.
XX
PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;
XX
DR WPI; 1986-106663/16.
DR N-PSDB; AAN60494.
XX
PT Vectors contg. gene for protein having erythroid potentiating activity -
PT used for producing protein to stimulate growth and formation of erythroid
PT cells.
XX
PS Disclosure; Fig 4; 59pp; English.
XX
CC The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)
CC and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a
CC biological activity of at least about 1,000,000 units per mg of protein
CC and has an apparent molecular weight of about 28,000 daltons
XX
SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

RESULT 2
AAP60275
ID AAP60275 standard; protein; 207 AA.
XX
AC AAP60275;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 08-AUG-1991 (first entry)
XX
DE Sequence of human natural inhibitor of collagenases (NIC).
XX
KW Metallo-proteinase inhibitor; wound healing; emphysema;
KW rheumatoid arthritis therapy; ulceration; tumour metastasis.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .23
FT		/label= signal
FT	Protein	24. .207
FT		/note= "claimed"
FT	Modified-site	53. .55
FT		/note= "potential glycosylation site"
FT	Modified-site	101. .103
FT		/note= "potential glycosylation site"

XX
PN EP189784-A.
XX
PD 06-AUG-1986.
XX
PF 16-JAN-1986; 86EP-00100482.
XX
PR 18-JAN-1985; 85US-00692808.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Galloway WA, Clissold PM, Mccullagh KG;
XX
DR WPI; 1986-205910/32.
DR N-PSDB; AAN60277.
XX
PT New human natural inhibitor of collagenase - for treating e.g. rheumatoid
PT arthritis or ulceration, and new DNA sequences coding for it.
XX
PS Disclosure; Fig 2; 51pp; English.
XX
CC The patentors claim the AA SQ of human NIC, DNA sequences coding for NIC,
CC and its RNA analogues and plasmids contg. this DNA. NIC inhibits the
CC activity of metallo-proteinases, esp. of collagenase, proteoglycanase,
CC gelatinase or a leucocyte, macrophage or tumour cell metallo-proteinase.
CC (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

RESULT 3
AAP60786
ID AAP60786 standard; protein; 207 AA.
XX
AC AAP60786;
XX
DT 25-MAR-2003 (revised)
DT 08-AUG-1991 (first entry)
XX
DE Sequence of tissue inhibitor of metalloproteinase (TIMP).
XX
KW Connective tissue; extracellular matrix.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .23
FT		/label= signal
FT	Protein	24. .207
FT	Modified-site	53. .55
FT		/label= potential N-glycosylation site
FT	Modified-site	101. .103
FT		/label= as above

XX
PN GB2169295-A.
XX
PD 09-JUL-1986.
XX
PF 06-JAN-1986; 86GB-00000199.
XX
PR 05-OCT-1983; 83BE-00897924.
PR 07-JAN-1985; 85GB-00000341.
PR 07-JAN-1985; 85GB-00500341.
PR 01-NOV-1985; 85GB-00026951.
XX
PA (CLLT) CELLTECH LTD.
XX
PI Harris TJR, Reynolds JJ, Docherty AJP, Murphy G;
XX
DR WPI; 1986-177873/28.
DR N-PSDB; AAN60538.
XX
PT Prodn. of metallo-proteinase inhibitors - by recombinant DNA techniques.
XX
PS Disclosure; Fig 3; 16pp; English.
XX
CC A gene with residues 64-684 of AAN60538 is claimed. AAN60538 was isolated
CC from human a foetal diploid lung cells (ATCC CLL153) cDNA library using
CC AAN60539. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 207 AA;

```
  Query Match             100.0%;  Score 1124;  DB 1;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 4
AAW30309
ID   AAW30309 standard; protein; 207 AA.
XX
AC   AAW30309;
XX
DT   29-JAN-1998  (first entry)
XX
DE   Human TIMP-1.
XX
KW   TIMP-3; human; antibody; TIMP-3-mediated disease; malignant tumour cell;
KW   cancer progression; TIMP-1.
XX
OS   Homo sapiens.
XX
PN   JP09235300-A.
XX
PD   09-SEP-1997.
XX
PF   29-FEB-1996;   96JP-00067484.
XX
PR   29-FEB-1996;   96JP-00067484.
XX
PA   (FUJY ) FUJI PHARM IND CO LTD.
XX
DR   WPI; 1997-498341/46.
DR   N-PSDB; AAT92631.
XX
PT   Human TIMP-3 and anti-human TIMP-3 monoclonal antibodies - used in
PT   diagnosis of TIMP-3 mediated diseases, especially the detection of
PT   malignant tumour cells.
XX
PS   Example 12; Page 33-34; 37pp; Japanese.
XX
CC   This sequence represents the human TIMP-1 protein. This sequence was used
CC   to test the specificity of the monoclonal antibody (MAb) of the
CC   invention. The MAb of the invention reacts specifically with human TIMP-3
CC   (see AAW30308), by specific recognition of the TIMP-3 fragments
CC   represented by AAW30305-W30307. The MAb can be used in the study or
CC   diagnosis of TIMP-3-mediated diseases, particularly for the detection of
CC   malignant tumour cells, or the diagnosis of progressiveness of cancers.
CC   They can also be used in establishing an immunoassay for TIMP-3 or in
CC   purification of TIMP-3. The transformed cells can be used for producing
CC   TIMP-3 or its equivalent proteins on a large scale. The immunoassay
CC   method for TIMP-3 the MAbs is simple, highly reproducible and highly
CC   sensitive
XX
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 5
AAY08933
ID   AAY08933 standard; protein; 207 AA.
XX
AC   AAY08933;
XX
DT   19-AUG-1999  (first entry)
XX
DE   Human TIMP-1 protein.
XX
KW   TIMP-4; tissue inhibitor of metalloprotease; human; antibody; diagnosis;
KW   treatment; metastasis; neoplastic cell; angiogenesis; tumour; cervical;
KW   uterine; pancreatic; colon; intestinal carcinoma; pregnancy; ulcer;
KW   osteoarthritis; pulmonary emphysema; peridontal disease; corneal;
KW   rheumatoid arthritis; diabetic ulcer; lesion; TIMP-4.
XX
OS   Homo sapiens.
XX
PN   US5914392-A.
XX
PD   22-JUN-1999.
XX
PF   07-JUL-1998;   98US-00111070.
XX
PR   18-JAN-1996;   96US-00588163.
PR   27-JUN-1997;   97US-00884073.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Murry LE,  Hawkins PR;
XX
DR   WPI; 1999-384187/32.
XX
PT   Anti-tissue inhibitor metalloproteinase antibodies useful for treating
PT   and diagnosing cancer.
XX
PS   Disclosure; Fig 4; 26pp; English.
XX
CC   This invention describes a novel method for the production of antibodies
CC   specific for the human tissue inhibitors of metalloproteinase 4, TIMP-4.
CC   The anti-TIMP-4 antibodies may be used to treat, prevent or diagnose
CC   metastasis of neoplastic cells, angiogenesis and growth tumours such as
CC   cervical, uterine, pancreatic, colon or intestinal carcinomas, pregnancy,
CC   osteoarthritis, pulmonary emphysema, peridontal disease, rheumatoid
CC   arthritis, corneal or diabetic ulcers or ulcers and lesions caused by
CC   microorganisms. This sequence represents TIMP-4 which is used to describe
CC   the method of the invention
XX
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 2;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

```
RESULT 6
AAB19073
ID   AAB19073 standard; protein; 207 AA.
XX
AC   AAB19073;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Inhibitor of tissue metalloproteinase designated TIMP-1.
XX
KW   Tissue metalloproteinase inhibitor; TIMP; metalloproteinase; gelatinase;
KW   metastasis; cancer.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /note= "signal peptide"
FT   Protein         24. .207
FT                   /note= "mature protein"
XX
PN   EP1041083-A1.
XX
PD   04-OCT-2000.
XX
PF   03-APR-2000; 2000EP-00107041.
XX
PR   01-APR-1999;   99JP-00095142.
XX
PA   (ORIY ) ORIENTAL YEAST CO LTD.
XX
PI   Miyazaki K,  Higashi S;
XX
DR   WPI; 2000-603818/58.
XX
PT   New modified tissue inhibitor of metalloproteinases, useful for
PT   manufacturing compositions for inhibiting metastasis of cancer and
PT   vascularization and for preventing or treating diseases associated with
PT   these, e.g. brain tumor.
XX
PS   Disclosure; Page 12-13; 25pp; English.
XX
CC   The present sequence represents an inhibitor of tissue metalloproteinase,
CC   designated TIMP. The specification describes modified forms of TIMP,
CC   where the amino-terminal alpha-amino group is modified with an electron
CC   accepting group to substantially lose the ability to bind to a
CC   metalloproteinase. Modified TIMP-2 prevents an accumulation of active
CC   gelatinase. A on the cell surface, and can inhibit the activation of
CC   precursor matrix matelloproteinases. The modified TIMP-2 and the
CC   compositions comprising TIMP-2 are useful for inhibiting metastasis of
CC   cancer and vascularisation. It is also used for treating diseases
CC   associated with them. Specifically, these are useful for preventing or
CC   treating metastasis of cancer of the stomach, colon, lung, head and neck,
CC   brain tumour, breast, thyroid, prostate, ovary or pancreas, or
CC   vascularisation or other conditions associated with these
XX
SQ   Sequence 207 AA;
```

```
  Query Match           100.0%;  Score 1124;  DB 3;  Length 207;
  Best Local Similarity  100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

```
RESULT 7
ADC37139
ID   ADC37139 standard; protein; 207 AA.
XX
AC   ADC37139;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human tissue inhibitor of metalloproteinase-1 (TIMP-1) protein.
XX
KW   liver fibrosis; alpha-2-macroglobulin; alpha-2-MG; hyaluronic acid; HA;
KW   tissue inhibitor of metalloproteinases-1; TIMP-1; anti-fibrotic therapy;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2003073822-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006038.
XX
PR   28-FEB-2002; 2002US-00087188.
XX
PA   (PROM-) PROMETHEUS LAB INC.
XX
PI   Rose SL,  Oh EH,  Walsh MJ;
XX
DR   WPI; 2003-756744/71.
DR   N-PSDB; ADC37138.
XX
PT   Diagnosing the presence or severity of liver fibrosis in an individual by
PT   detecting alpha2-macroglobulin, hyaluronic acid or detecting tissue
PT   inhibitor of metalloproteinases-1 in a sample from the individual.
XX
PS   Disclosure; SEQ ID NO 4; 133pp; English.
XX
CC   The invention relates to a novel method for diagnosing the presence or
CC   severity of liver fibrosis in an individual. The novel method comprises:
CC   detecting alpha-2-macroglobulin (alpha-2-MG) in a sample from the
CC   individual; detecting hyaluronic acid (HA) in a sample from the
CC   individual; detecting tissue inhibitor of metalloproteinases-1 (TIMP-1)
CC   in a sample from the individual; and diagnosing the presence or severity
CC   of liver fibrosis in the individual based on the presence or level of
CC   alpha-2-MG, HA and TIMP-1. The methods are useful for diagnosing the
CC   presence or severity of liver fibrosis in an individual, differentiating
CC   no or mild liver fibrosis in an individual to severe liver fibrosis, and
CC   monitoring the efficacy of anti-fibrotic therapy in a patient. This
CC   sequence represents the human tissue inhibitor of metalloproteinase-1
CC   (TIMP-1) protein of the invention.
XX
```

```
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 7;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 8
ADL78829
ID   ADL78829 standard; protein; 207 AA.
XX
AC   ADL78829;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human tissue inhibitor of metalloproteinase-1 (TIMP-1).
XX
KW   vasotropic; antiasthmatic; dermatological; nephrotropic; antirheumatic;
KW   antiarthritic; antipsoriatic; osteopathic; cytostatic; vulnerary;
KW   antithyroid; antiulcer; neuroprotective; antibacterial;
KW   immunosuppressive; metalloproteinase inhibitor;
KW   tissue inhibitor of metalloproteinase 4; TIMP-4; restenosis; arthritis;
KW   soft tissue rheumatism; polychondritis; tendonitis;
KW   bone resorption disease; osteoporosis; Paget's disease; hyperthyroidism;
KW   cholesteatoma; collagen destruction; diabetes;
KW   dystrophic epidermolysis bullosa; periodontal disease; alveolitis;
KW   gingival production of collagenase; corneal ulceration; skin ulceration;
KW   gastro-intestinal tract ulceration; wound healing; cancer;
KW   demyelinating disease; asthma; glomerulosclerosis; septic shock;
KW   infection; psoriasis; human; TIMP-1;
KW   Tissue inhibitor of metalloproteinase 1.
XX
OS   Homo sapiens.
XX
PN   US2003157687-A1.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003US-00366445.
XX
PR   13-DEC-1994;   94WO-US014498.
PR   05-JUN-1995;   95US-00463261.
PR   01-SEP-1999;   99US-00387525.
PR   11-JUL-2000; 2000US-0217419P.
PR   26-JUL-2000; 2000US-0220829P.
PR   11-JUL-2001; 2001US-00901904.
XX
PA   (GREE/) GREENE J M.
PA   (ROSE/) ROSEN C A.
XX
PI   Greene JM,  Rosen CA;
XX
DR   WPI; 2003-897817/82.
XX
PT   New polynucleotide encoding a tissue inhibitor of metalloproteinase
PT   designated TIMP-4 is useful to treat metalloproteinase associated disease
PT   including restenosis and collagenase-associated disease.
XX
PS   Disclosure; Fig 2; 61pp; English.
XX
CC   The invention describes an isolated polynucleotide encoding a tissue
CC   inhibitor of metalloproteinase designated TIMP-4. The invention is used
CC   to treat restenosis. Other disease which may be treated include arthritic
CC   diseases such as rheumatoid and osteoarthritis, soft tissue rheumatism,
CC   polychondritis and tendonitis, bone resorption diseases such as
CC   osteoporosis, Paget's disease, hyperthyroidism and cholesteatoma, the
CC   enhanced collagen destruction that occurs with diabetes, the recessive
CC   classes of dystrophic epidermolysis bullosa, periodontal disease,
CC   alveolitis and related consequences of gingival production of
CC   collagenase, corneal ulceration, ulceration of the skin and gastro-
CC   intestinal tract and abnormal wound healing, post-operative conditions in
CC   which collagenase levels are raised, cancer by blocking the destruction
CC   of tissue basement membranes leading to cancer metastases, demyelinating
CC   disease of the central and peripheral nervous systems, asthma,
CC   glomerulosclerosis, septic shock and infection, and psoriasis. This is
CC   the amino acid sequence of human tissue inhibitor of metalloproteinase-1
CC   (TIMP-1) used in a comparison with TIMP-4 of the invention.
XX
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 7;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 9
ADG25251
ID   ADG25251 standard; protein; 207 AA.
XX
AC   ADG25251;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human TIMP-1 #SEQ ID 20.
XX
KW   Antiinflammatory; hypotensive; antiallergic; immunosuppressive;
KW   antiasthmatic; protease; lipase; inhibitor; lung surfactant;
KW   pulmonary inflammation; emphysema; pneumonia; human.
XX
OS   Homo sapiens.
XX
PN   WO2003090682-A2.
XX
PD   06-NOV-2003.
XX
PF   25-APR-2003; 2003WO-US012731.
XX
PR   25-APR-2002; 2002US-0375968P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Cochrane CG,  Oades ZG,  Revak SD,  Niven R;
XX
DR   WPI; 2004-132634/13.
```

```
XX
PT   Composition useful for treating pulmonary inflammation e.g. chronic
PT   obstructive pulmonary disease comprises a lung surfactant polypeptide and
PT   a protease inhibitor.
XX
PS   Claim 6; SEQ ID NO 20; 137pp; English.
XX
CC   The invention relates to a liquid aerosolised composition, comprising a
CC   lung surfactant polypeptide and a protease inhibitor. The composition is
CC   useful for treating pulmonary inflammation (e.g. inflammation associated
CC   with pulmonary hypertension, neonatal pulmonary hypertension, neonatal
CC   bronchopulmonary dysplasia, chronic obstructive pulmonary disease, acute
CC   or chronic bronchitis, emphysema, bronchiolitis, bronchiectasis,
CC   radiation pneumonitis, hypersensitivity, pneumonitis, acute inflammatory
CC   asthma, acute smoke inhalation, thermal lung injury, allergic asthma,
CC   iatrogenic asthma, cystic fibrosis, alveolar proteinosis, alpha-1-
CC   protease deficiency, pulmonary inflammatory disorders, pneumonia, acute
CC   respiratory distress syndrome, acute lung injury, idiopathic respiratory
CC   distress syndrome, and idiopathic pulmonary fibrosis). The current
CC   sequence represents a protease inhibitor that may be part of a
CC   composition of the invention.
XX
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 8;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 10
ADQ07367
ID   ADQ07367 standard; protein; 207 AA.
XX
AC   ADQ07367;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human tissue inhibitor of metalloproteinase 1 (TIMP1).
XX
KW   matrix metalloproteinase; MMP; MMP inhibitor; proteinase inihibtor;
KW   scar prevention; skin development; human;
KW   tissue inhibitor of metalloproteinase 1; TIMP-1; wound healing; skin;
KW   enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004121438-A1.
XX
PD   24-JUN-2004.
XX
PF   19-DEC-2002; 2002US-00325446.
XX
PR   19-DEC-2002; 2002US-00325446.
XX
PA   (QUIR/) QUIRK S.
XX
PI   Quirk S;
XX
DR   WPI; 2004-479683/45.
XX
PT   New wound care compositions, useful in promoting wound healing,
PT   preventing scarring, improving skin tone, and in stimulating the
PT   development of a smooth, healthy skin.
XX
PS   Disclosure; SEQ ID NO 1; 43pp; English.
XX
CC   The invention describes an isolated nucleic acid (I). (I) comprises a
CC   sequence: encoding a polypeptide comprising a sequence of 108 amino acids
CC   (SEQ ID NOS: 5 or 20); or which hybridises under stringent hybridisation
CC   conditions to a nucleic acid comprising a sequence of 339 bp (SEQ ID NO:
CC   6). Also described are: an isolated polypeptide comprising SEQ ID NOS: 5
CC   or 20 or comprising SEQ ID NOS: 7 or 21 that has a beta barrel
CC   conformation and that can bind to a matrix metalloproteinase; a
CC   composition comprising a therapeutical amount of polypeptide or
CC   polypeptide inhibitor comprising SEQ ID NOS: 5, 7, 20 or 21 and a
CC   pharmaceutical carrier, where the polypeptide or polypeptide inhibitor
CC   can inhibit proteinase activity of matrix metalloproteinase-1 to -13; a
CC   wound dressing comprising a polypeptide of (1) and a pharmaceutical
CC   carrier; and treating a wound comprising administering a therapeutical
CC   amount of a polypeptide of (1) to the wound. (I) is nucleic acid
CC   comprising a sequence of 339 bp (SEQ ID NO: 6) encoding wound care
CC   compositions comprising a sequence of 108 amino acids (SEQ ID NOS: 5 or
CC   20). The nucleic acid and the encoded polypeptide, composition, and
CC   method are useful in promoting wound healing, preventing scarring,
CC   improving skin tone, and in stimulating the development of a smooth,
CC   healthy skin. This is the amino acid sequence of human tissue inhibitor
CC   of metalloproteinase 1 (TIMP-1), useful in wound healing and promoting
CC   development of healthy skin.
XX
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 8;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 11
ADP75947
ID   ADP75947 standard; protein; 207 AA.
XX
AC   ADP75947;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human TIMP1 protein diffferentially expressed in schizophrenics Seq 151.
XX
KW   tissue inhibitor of metalloproteinase 1; human; schizophrenia; SCYA2;
KW   GADD5B; S100A8; CDKN1A; IL1RL1; TGM2; MAFF; SERPINA3; GRO1; CD14;
KW   KIAA1075; CHI3L1; SERPINH1; MT1X; KIAA0620; TIMP1; NUMA1; DDIT3; TOB2;
KW   neuroleptic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2004053157-A2.
```

XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-EP014089.
XX
PR 12-DEC-2002; 2002US-0432853P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Buxton FP, Carpenter WT, Roberts RC, Tamminga CA;
XX
DR WPI; 2004-507015/48.
DR N-PSDB; ADP75928.
XX
PT Screening or diagnosing schizophrenia comprises determining the magnitude
PT of expression of at least one gene upregulated in the anterior cingulate.
XX
PS Example 2; SEQ ID NO 151; 63pp; English.
XX
CC Screening for schizophrenia in a population or diagnosing schizophrenia
CC in a host comprises determining the magnitude of expression, in members
CC of the population, of at least one of the 19 genes (SCYA2, GADD5B,
CC S100A8, CDKN1A, IL1RL1, TGM2, MAFF, SERPINA3, GRO1, CD14, KIAA1075,
CC CHI3L1, SERPINH1, MT1X, KIAA0620, TIMP1, NUMA1, DDIT3, or TOB2) in a
CC sample. Screening for schizophrenia in a population or diagnosing
CC schizophrenia in a host comprises: determining the magnitude of
CC expression, in members of the population, of at least one of the 19 genes
CC in a sample; and comparing the magnitude of expression to a baseline
CC magnitude of expression of the gene, where increased gene expression
CC indicates the presence of schizophrenia. INDEPENDENT CLAIMS are also
CC included for: treating schizophrenia in a host; a transgenic nonhuman
CC animal comprising stably integrated in its genome an increased copy
CC number of any of the 19 genes, where expression of the gene is enhanced
CC by one or more alterations in regulatory sequences of the gene such that
CC the gene is expressed at higher than baseline levels and the animal
CC exhibits schizophrenic behavior or a transgenic nonhuman knockout animal
CC whose genome comprises a homozygous disruption in one or more of the 19
CC genes, where the homozygous disruption prevents the expression of the
CC gene, and where the homozygous disruption results in the transgenic
CC knockout animal exhibiting decreased expression levels of the one or more
CC genes as compared to a wild-type animal; screening for a therapeutic
CC agent that modulates symptoms of schizophrenia; and screening for a
CC compound useful in treating schizophrenia. Preferred Method: The sample
CC is taken from brain, spinal cord, lymphatic fluid, blood, urine or feces.
CC The sample is taken from the anterior cingulate. The population or host
CC is human. Treating schizophrenia in a host comprises lowering expression
CC of at least one of the 19 genes by administering to the host: an
CC expression lowering amount of antisense oligonucleotide; an expression
CC lowering amount of a ribozyme which cleaves RNA associated with
CC expression of the gene; one or more nucleic acid molecules designed to
CC promote triple helix formation with the gene; or one or more RNAi
CC molecules designed to inhibit the expression of the gene. Alternatively,
CC the method comprises reducing the amount of at least one protein encoded
CC by any of the 19 genes in a patient by administering an amount of
CC antibody or functional antibody fragment to interfere with the normal
CC activity of the protein. The antibody or functional antibody fragment is
CC whole antibody, humanized antibody, chimeric antibody, Fab fragment, Fab'
CC fragment, F(ab')2 fragment, single chain Fv fragment, or diabody.
CC Screening for a therapeutic agent that modulates symptoms of
CC schizophrenia comprises administering a candidate compound to a
CC transgenic nonhuman animal of (2) or combining a candidate compound with
CC a transgenic nonhuman animal of (2) and determining the effect of the
CC compound on symptoms associated with schizophrenia. Screening for a
CC compound, useful in treating schizophrenia, comprises operatively linking
CC a reporter gene which expresses a detectable protein to a regulatory
CC sequence for any of the 19 genes to produce a reporter construct,
CC transfecting a cell with the reporter construct, exposing the transfected
CC cell to a test compound and comparing the level of expression of the
CC reporter gene before and after exposure to the test compound, where a
CC lower level of expression after exposure is indicative of a compound
CC useful for the treatment of schizophrenia. Preferred Transgenic Nonhuman
CC Animal: The transgenic nonhuman animal is a mammal. One or more
CC alterations comprise substitution of a promoter having a higher rate of
CC expression than the native promoter of the gene. The promoter is an
CC inducible promoter. Neuroleptic. No biological data given. Gene Therapy.
CC Dosage is 0.1-100000 &mgr;g/kg, by topical, pulmonary, intratracheal,
CC intranasal, enteral, epidermal and transdermal, oral, sublingual, buccal
CC or parenteral including intravenous, intraarterial, subcutaneous,
CC intraperitoneal, intramuscular, infusion, intramedullary, intracranial,
CC intrathecal or intraventricular means. The method is useful for screening
CC for schizophrenia in a population or diagnosing schizophrenia in a host.
CC The methods, compounds and compositions are useful in treating
CC schizophrenia.
XX
SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
Db 1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy 61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
Db 61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy 121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
Db 121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
Db 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207

RESULT 12
ADQ29674
ID ADQ29674 standard; protein; 207 AA.
XX
AC ADQ29674;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human colorectal cancer-associated protein #29.
XX
KW human; colon cancer; TIMP1; Reg1-alpha;
KW colorectal cancer-associated marker.
XX
OS Homo sapiens.
XX
PN EP1439393-A2.
XX
PD 21-JUL-2004.
XX
PF 15-DEC-2003; 2003EP-00257868.
XX
PR 13-DEC-2002; 2002US-0433554P.
PR 31-JUL-2003; 2003US-0491397P.
XX
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Astle JH, Boardman LA, Bugart LJ, Burgess CC, Catino TJ;
PI Dwivedi P, Huntress M, Johnson KA, Lewis ME, Maimonis PJ, Myerow SH;
PI Brown-Shimer SLA, Thiagalingam A, Thibodeau SN, Molino GA;
XX
DR WPI; 2004-545561/53.
DR N-PSDB; ADQ29607.
XX
PT Diagnosing colon cancer in individual, preferably human, by detecting
PT presence of TIMP 1 in sample, where presence of TIMP 1 in sample is
PT indicative of colon cancer in individual.

```
XX
PS   Claim 7; SEQ ID NO 100; 433pp; English.
XX
CC   The invention comprises a method for diagnosing colon cancer in an
CC   individual, the method involves obtaining a serum sample from the
CC   individual and detecting the presence of either TIMP1 or Reg1-alpha and
CC   an additional colorectal cancer-associated marker. The method of the
CC   invention is useful for diagnosing colon cancer in an individual. The
CC   present amino acid sequence represents a human colorectal cancer-
CC   associated protein of the invention.
XX
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 8;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 13
ADP23249
ID   ADP23249 standard; protein; 207 AA.
XX
AC   ADP23249;
XX
DT   18-NOV-2004  (first entry)
XX
DE   PRO polypeptide SEQ ID NO:343.
XX
KW   PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW   osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW   antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS   Unidentified.
XX
PN   WO2004041170-A2.
XX
PD   21-MAY-2004.
XX
PF   30-OCT-2003; 2003WO-US034312.
XX
PR   01-NOV-2002; 2002US-0423394P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Clark H,  Schoenfeld J,  Van Lookeren M,  Williams PM,  Wood WI;
PI   Wu TD;
XX
DR   WPI; 2004-419628/39.
DR   N-PSDB; ADP23248.
XX
PT   New PRO polypeptides and polynucleotides, useful for treating e.g.
PT   erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT   renal disease, or demyelinating diseases of the central or peripheral
PT   nervous system.
XX
PS   Claim 7; SEQ ID NO 343; 2940pp; English.
XX
CC   The invention relates to a novel isolated nucleic acid and the PRO
CC   polypeptide encoded by it. A protein of the invention has
CC   antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC   osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC   antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC   of the invention may have a use in gene therapy. The PRO polypeptide, its
CC   agonist, antagonist, or antibody that specifically binds to the
CC   polypeptide is useful for treating an immune related disorder such as
CC   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC   juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC   idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC   vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC   thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC   disease, a demyelinating disease of the central or peripheral nervous
CC   system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC   a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC   disease, infectious or autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC   inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC   disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC   disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC   disease, asthma, allergic rhinitis, atopic dermatitis, food
CC   hypersensitivity, urticaria, an immunologic disease of the lung,
CC   eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC   pneumonitis, a transplantation associated disease, graft rejection or
CC   graft-versus-host disease. The present sequence represents a PRO protein
CC   of the invention.
XX
SQ   Sequence 207 AA;

  Query Match             100.0%;  Score 1124;  DB 8;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-109;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207


RESULT 14
ADU06696
ID   ADU06696 standard; protein; 207 AA.
XX
AC   ADU06696;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Novel bronchial cancer-associated human protein SeqID922.
XX
KW   bronchial cancer; cytostatic; tumour-associated protein;
KW   cancer detection; metastasis; tumour; human.
XX
OS   Homo sapiens.
XX
PN   DE10316701-A1.
XX
PD   04-NOV-2004.
XX
PF   09-APR-2003; 2003DE-01016701.
XX
PR   09-APR-2003; 2003DE-01016701.
```

XX
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
XX
PI Mennerich D, Bruemmendorf T, Heiden E, Hermann K, Kinnemann H;
PI Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;
XX
DR WPI; 2004-786403/78.
DR N-PSDB; ADU06209.
XX
PT New nucleic acid, and derived proteins, useful for diagnosis of bronchial
PT cancer and in screening for therapeutic and diagnostic agents.
XX
PS Claim 2; SEQ ID NO 922; 1381pp; German.
XX
CC This invention relates to a novel isolated nucleic acid associated with
CC bronchial cancer comprising 489 defined sequences given in the
CC specification. The invention may be useful for the production of
CC compounds with a cytostatic activity through the inhibition of expression
CC or activity of tumour-associated proteins. The novel DNA sequences and
CC the proteins/peptides encoded by them are used for detecting bronchial
CC cancer or determining the risk of developing it and to screen for
CC specific binding partners of the DNA or protein sequences, where the
CC binding partners are potentially useful as agents for treating or
CC diagnosing bronchial cancer. The DNA or protein sequences can also be
CC used for prognosis, detection of metastases and for secondary treatment
CC (of tumours that have been stabilised or are no longer detectable).
CC Detecting abnormal expression of the DNA sequences provides early
CC diagnosis of bronchial cancers. The present sequence is that of a protein
CC encoded by a novel bronchial cancer-associated human gene sequence of the
CC invention.
XX
SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
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Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
```

RESULT 15
ADV70205
ID ADV70205 standard; protein; 207 AA.
XX
AC ADV70205;
XX
DT 10-MAR-2005 (first entry)
XX
DE Tumor-associated antigenic target polypeptide TAT447.
XX
KW cytostatic; diagnosis; therapy; tumor;
KW tumor-associated antigenic target polypeptide; TAT.
XX
OS Homo sapiens.
XX
PN WO2004112829-A2.
XX
PD 29-DEC-2004.
XX
PF 21-MAY-2004; 2004WO-US016121.
XX
PR 23-MAY-2003; 2003US-0473238P.
PR 27-FEB-2004; 2004US-0548299P.
XX
PA (GETH) GENENTECH INC.
XX
PI Phillips H;
XX
DR WPI; 2005-048766/05.
DR N-PSDB; ADV70110.
XX
PT Treating a mammal having a tumor of glial origin comprising cells that
PT express a type A or B glial tumor antigen by contacting the cells with a
PT composition comprising first and second binding agents.
XX
PS Disclosure; SEQ ID NO 129; 374pp; English.
XX
CC The invention describes a method of treating a mammal having a tumor of
CC glial origin comprising cells that express a type A or B glial tumor
CC antigen comprises contacting the cells with a composition of: a first
CC binding agent comprising a first antibody, oligopeptide or organic
CC molecule that binds to a type A or B glial tumor antigen; and a second
CC binding agent comprising a second antibody, oligopeptide or organic
CC molecule that binds to a type B or A glial tumor antigen. Also described
CC is a method of determining the presence of a type A or B glial tumor in a
CC mammal. The method is useful in treating a mammal having a tumor of glial
CC origin comprising cells that express a type A or B glial tumor antigen.
CC This sequence represents a human tumor-associated antigenic target
CC polypeptide.
XX
SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 9; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPFEPLASGILLLLWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQR 60

Qy         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHIT 120

Qy        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEK 180

Qy        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
              |||||||||||||||||||||||||||
Db        181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
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Job time : 84.203 secs

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